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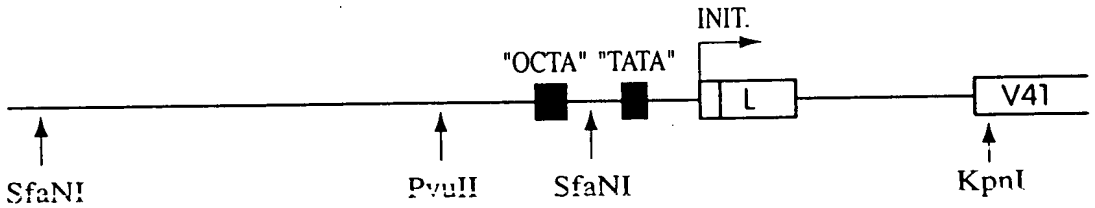


MOPC-41 κ CHAIN GENE

Fig. 1A

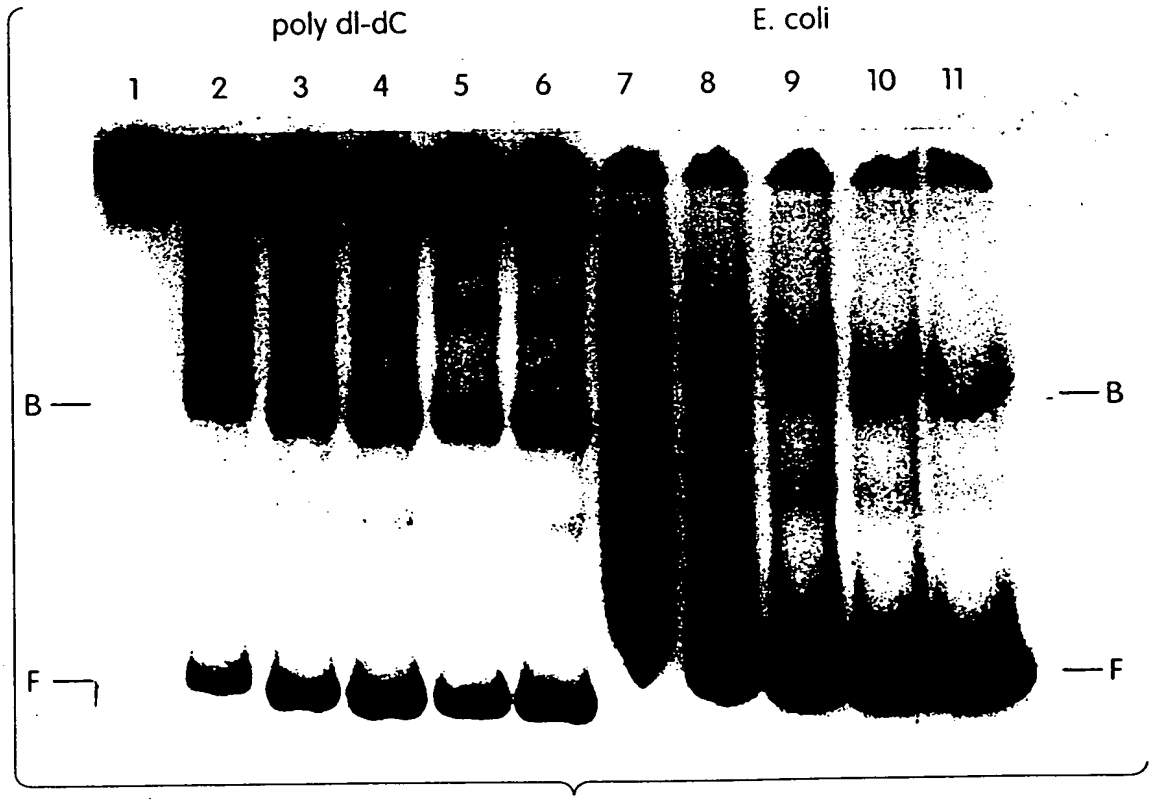


Fig. 1B

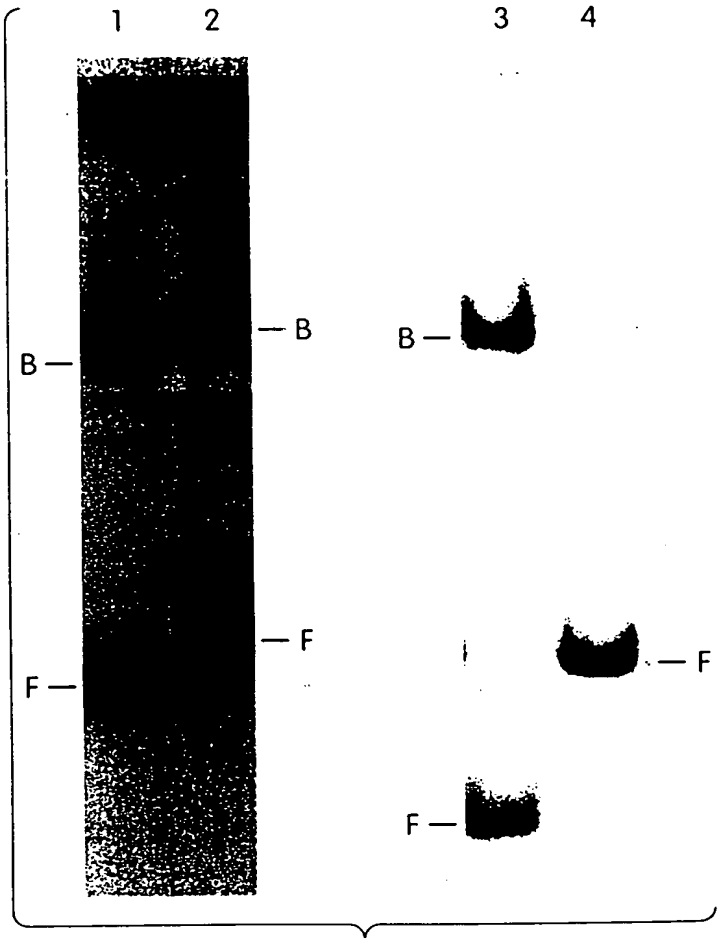


Fig. 1C

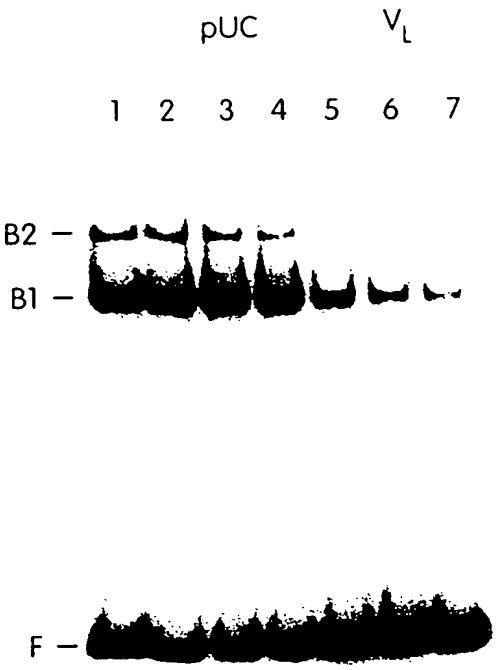


Fig. 2A

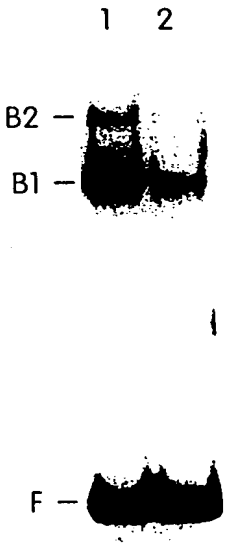


Fig. 2B

Fig. 3

	* *
V_L coding strand (-66)	TCTTAATA ATTTGCAT ACCCTCAC
V_H non-coding strand (-50)	CGCACATG ATTTGCAT ACTCATGA
J_H - Cμ coding strand (166)	CCTGGGTA ATTTGCAT TTCTAAAA

Fig. 4A

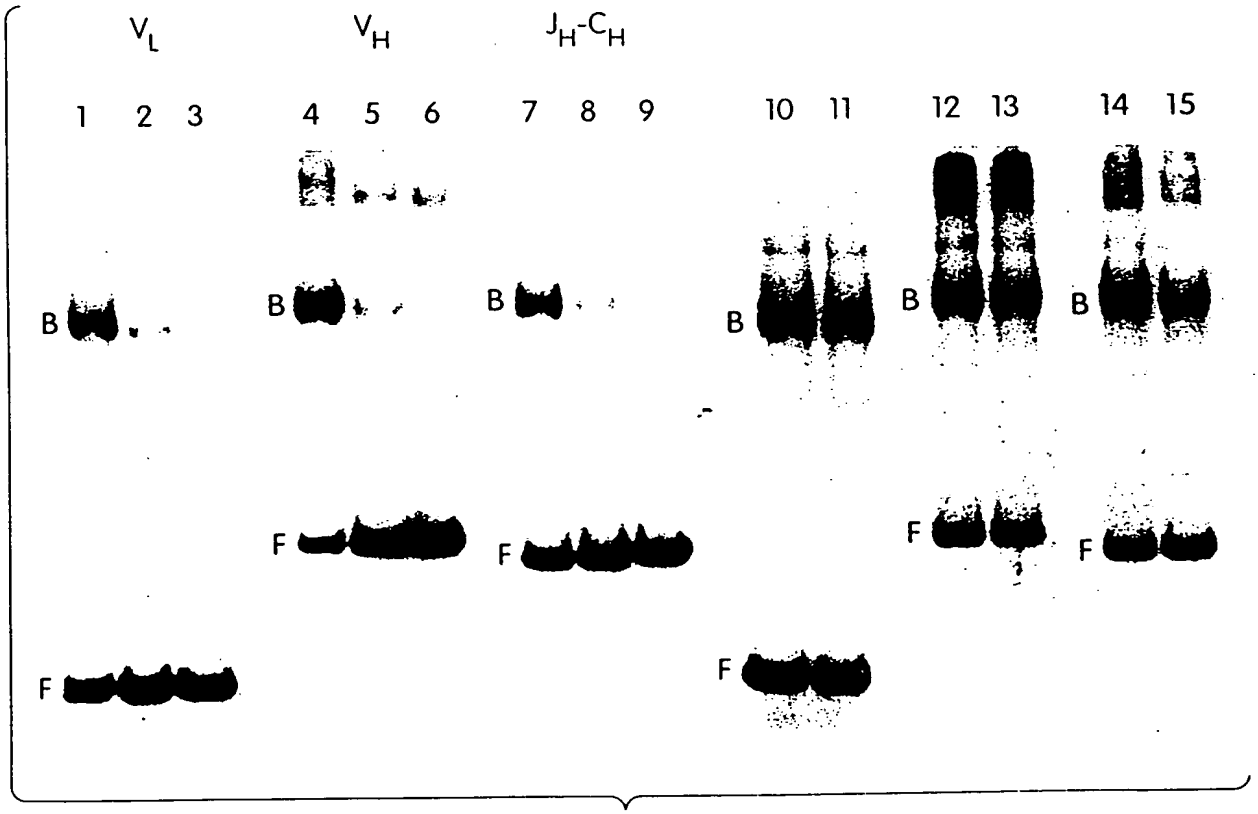


Fig. 4B

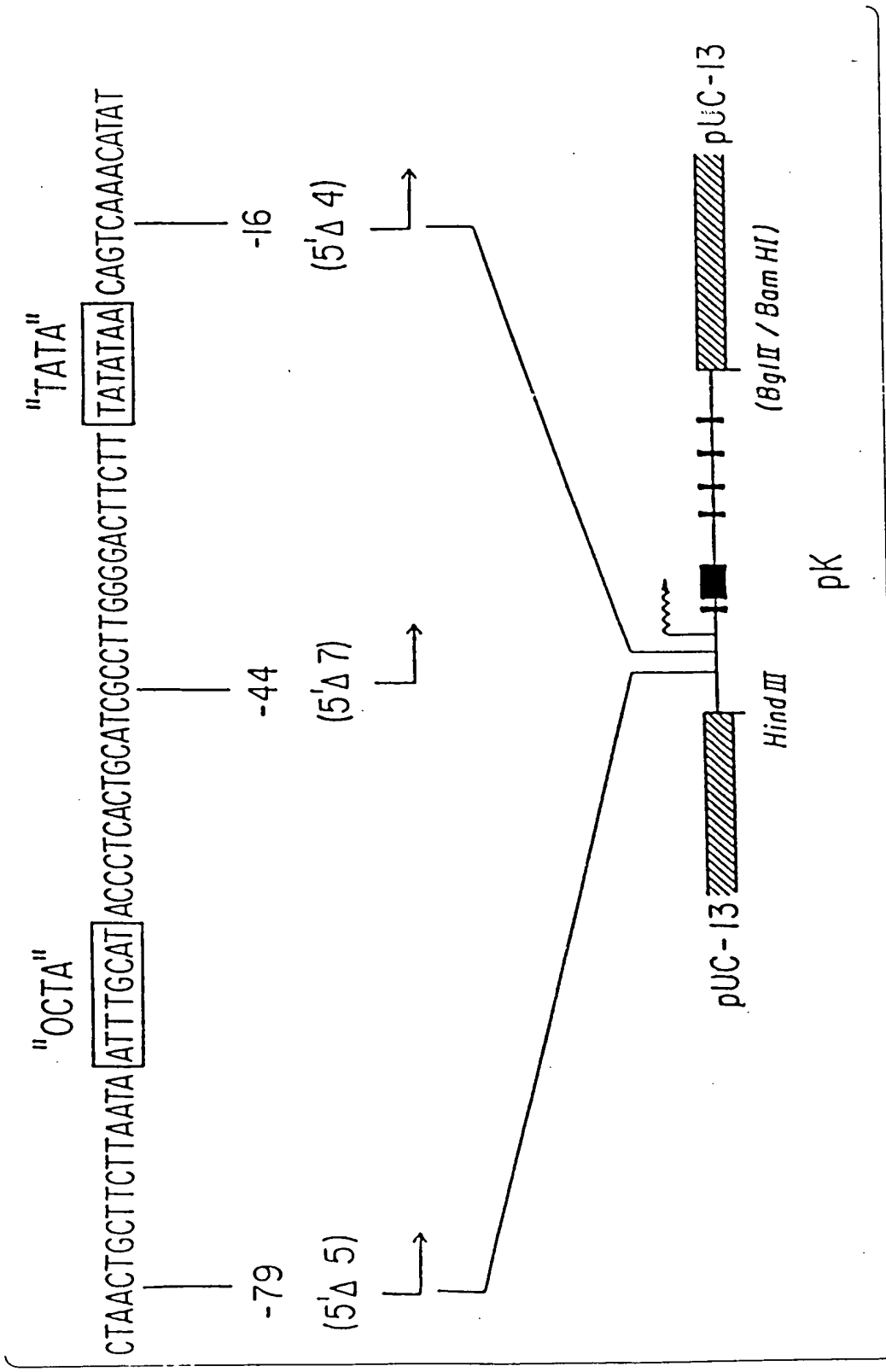

"OCTA"
"TATA"
CTAACTGCTTCTTAATA ATTTGCAT ACCCTCACTGCATCGCCTTGGGGACTTCTT TATATAA CAGTCAAACATAT
-79
-44
-16
(5'Δ 5)
(5'Δ 7)
(5'Δ 4)
pUC-13
Hind III
(BglII / Bam HI)
pUC-13
pK

Fig. 5A

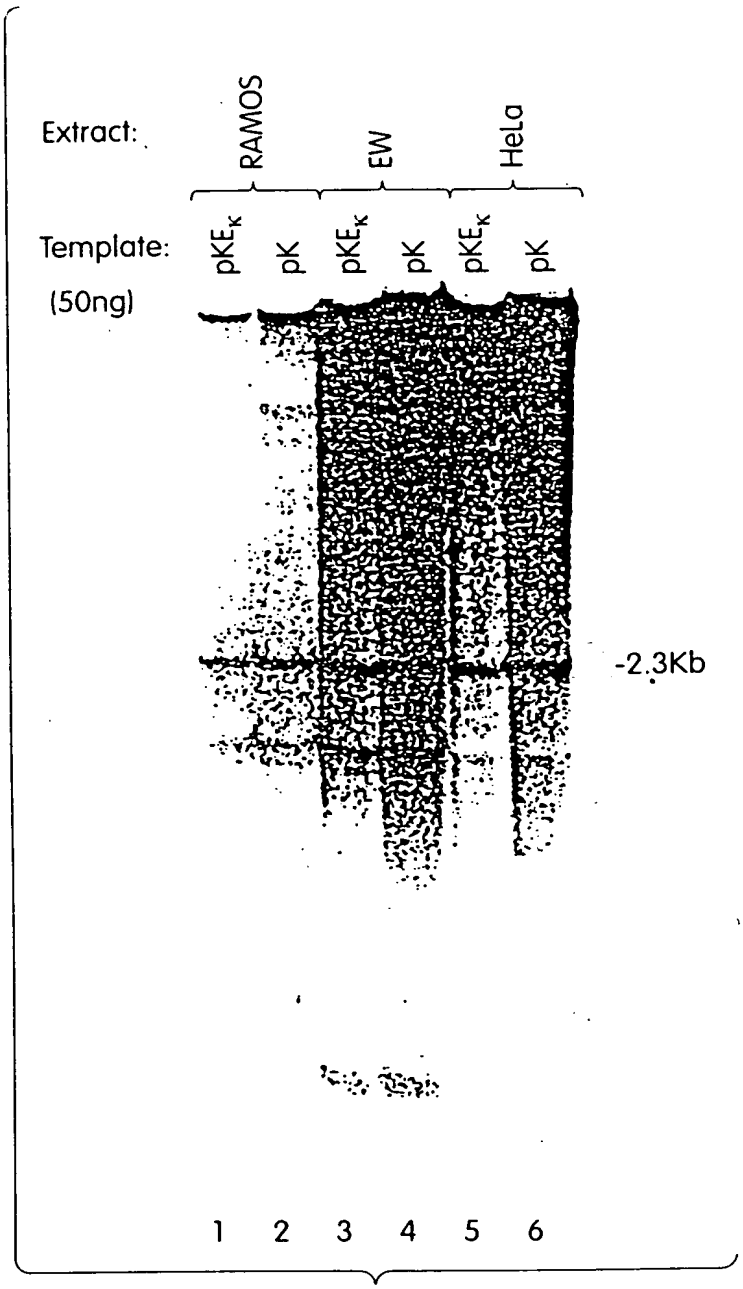

Extract:
RAMOS
EW
HeLa
Template:
(50ng)
pKE$_\kappa$
pK
pKE$_\kappa$
pK
pKE$_\kappa$
pK
-2.3Kb
1 2 3 4 5 6

Fig. 5B

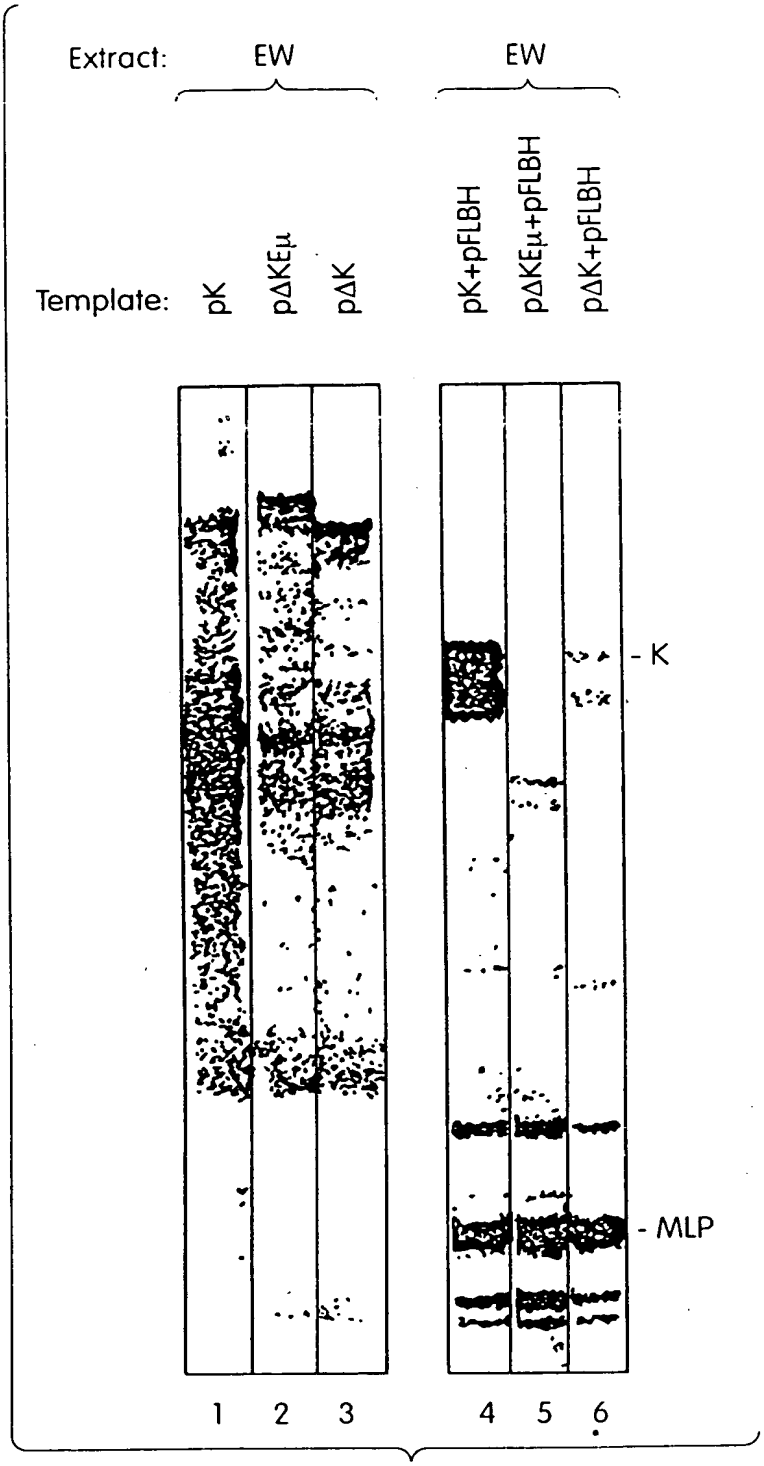

Extract:
EW
EW
Template:
pK
pΔKEμ
pΔK
pK+pFLBH
pΔKEμ+pFLBH
pΔK+pFLBH
- K
- MLP
1
2
3
4
5
6

Fig. 6

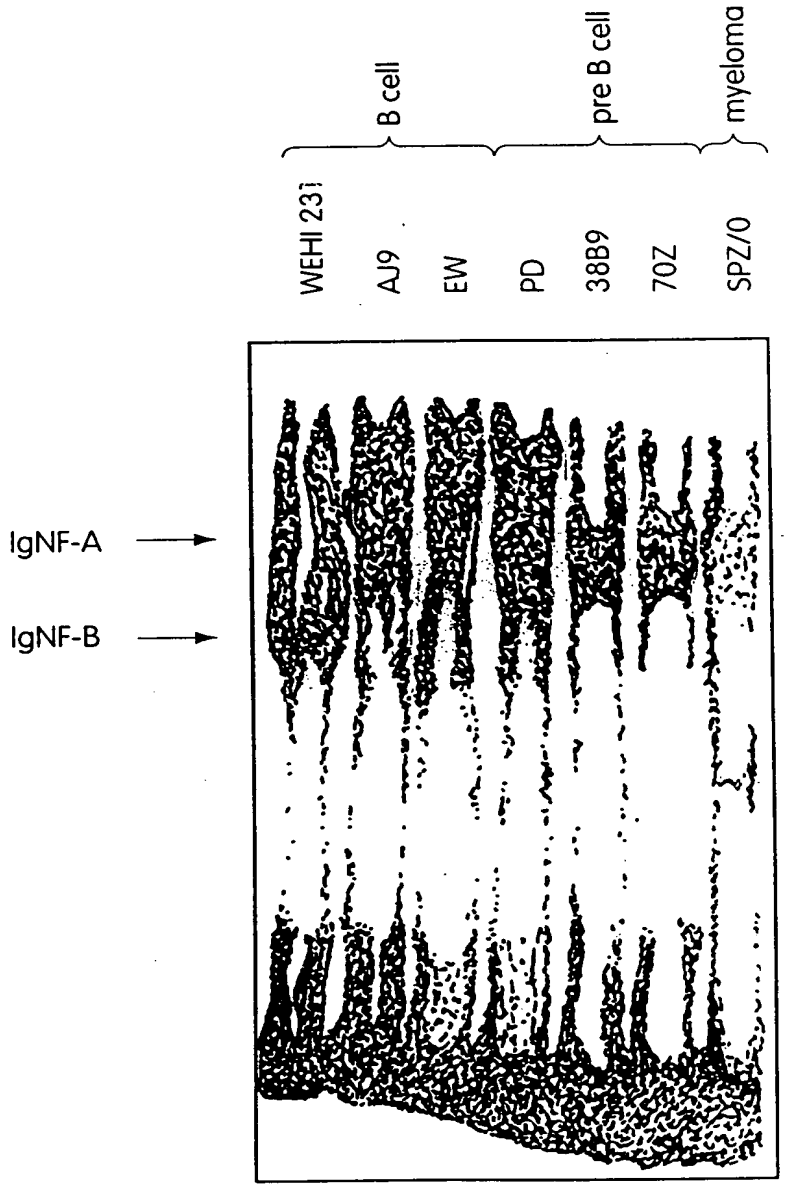

B cell
pre B cell
myeloma
WEHI 231
AJ9
EW
PD
38B9
70Z
SPZ/0
IgNF-A
IgNF-B

Fig. 7

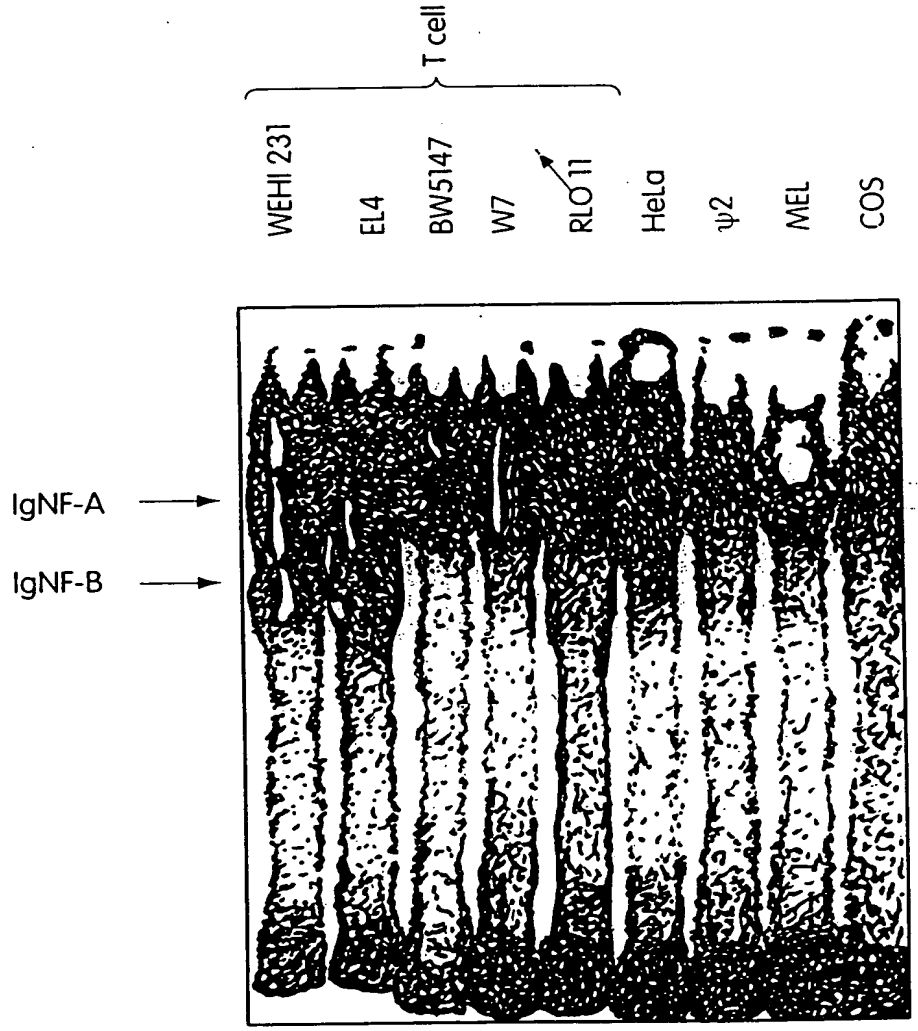
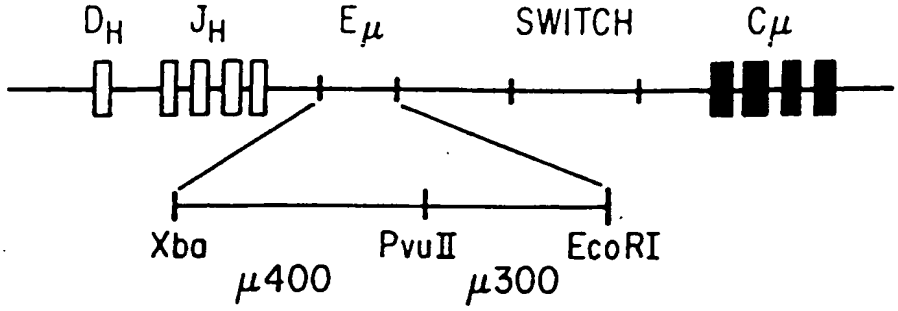

T cell
WEHI 231
EL4
BW5147
W7
RLO 11
HeLa
ψ2
MEL
COS
IgNF-A
IgNF-B

Fig. 8

Figure 9A



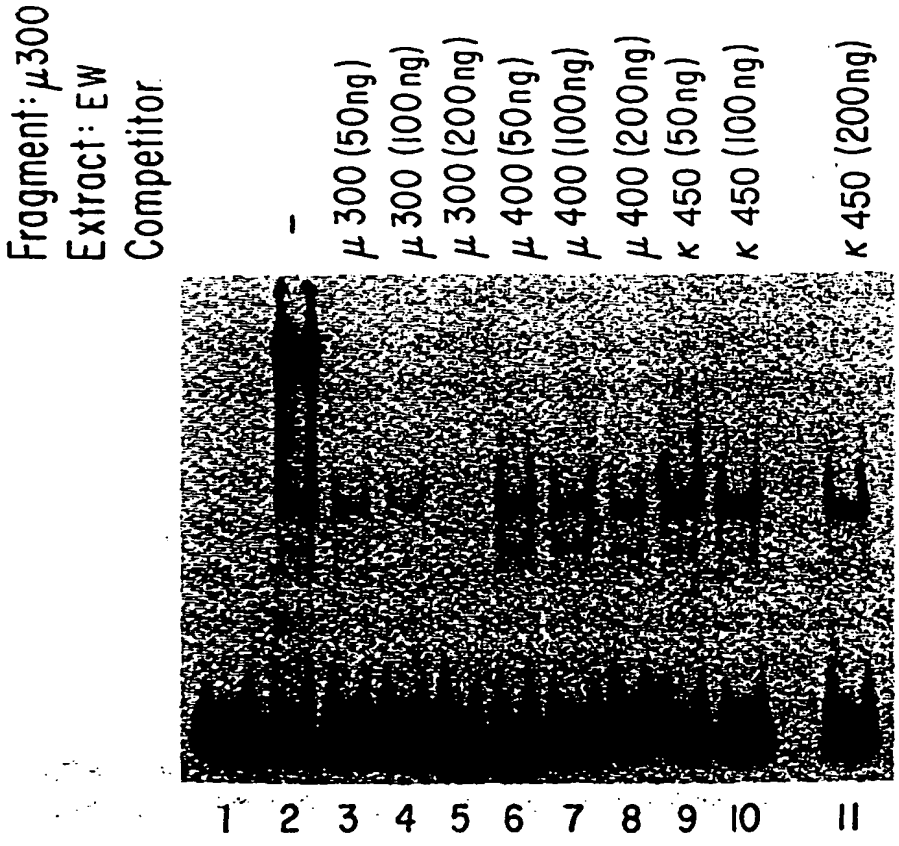


Figure 9B

Figure 10A

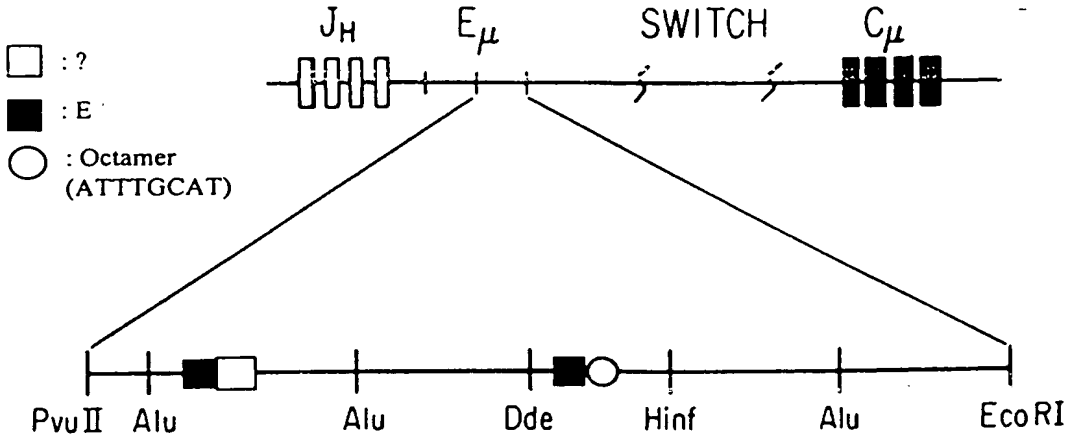
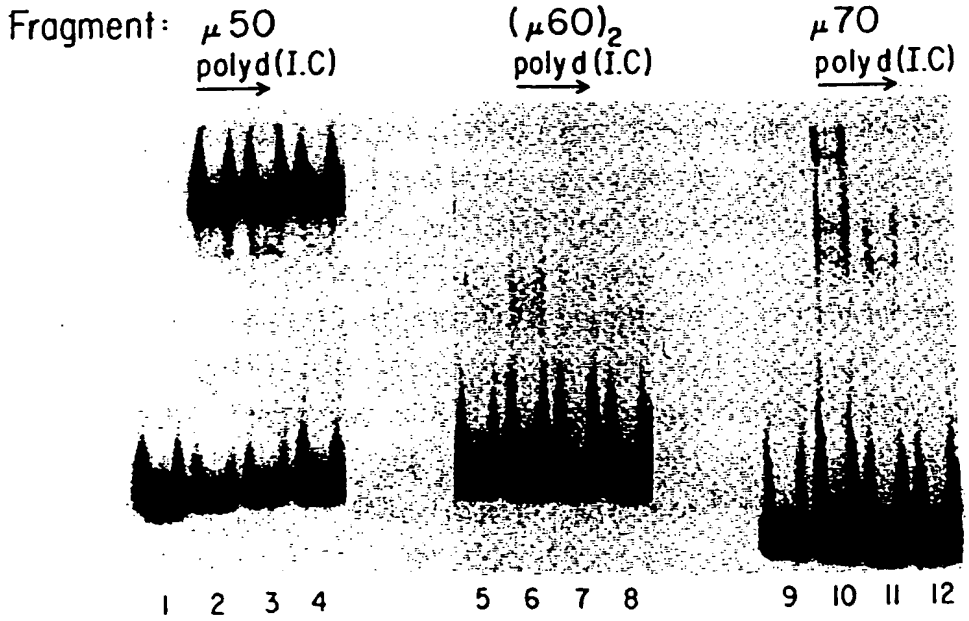


Figure 10B



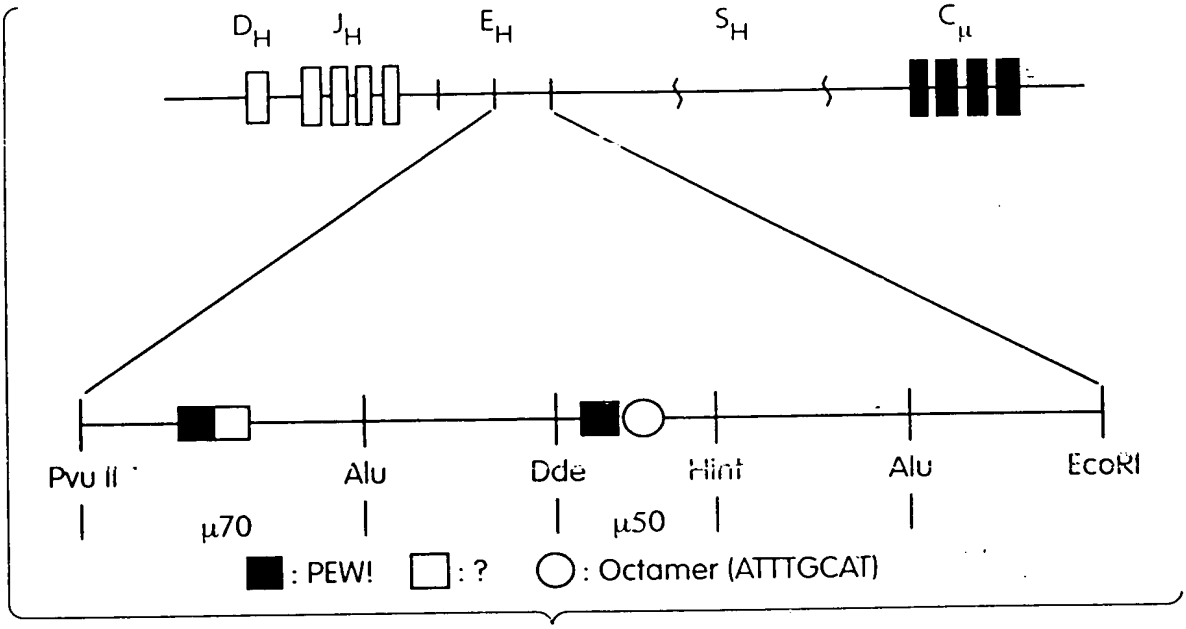


Fig. 10C

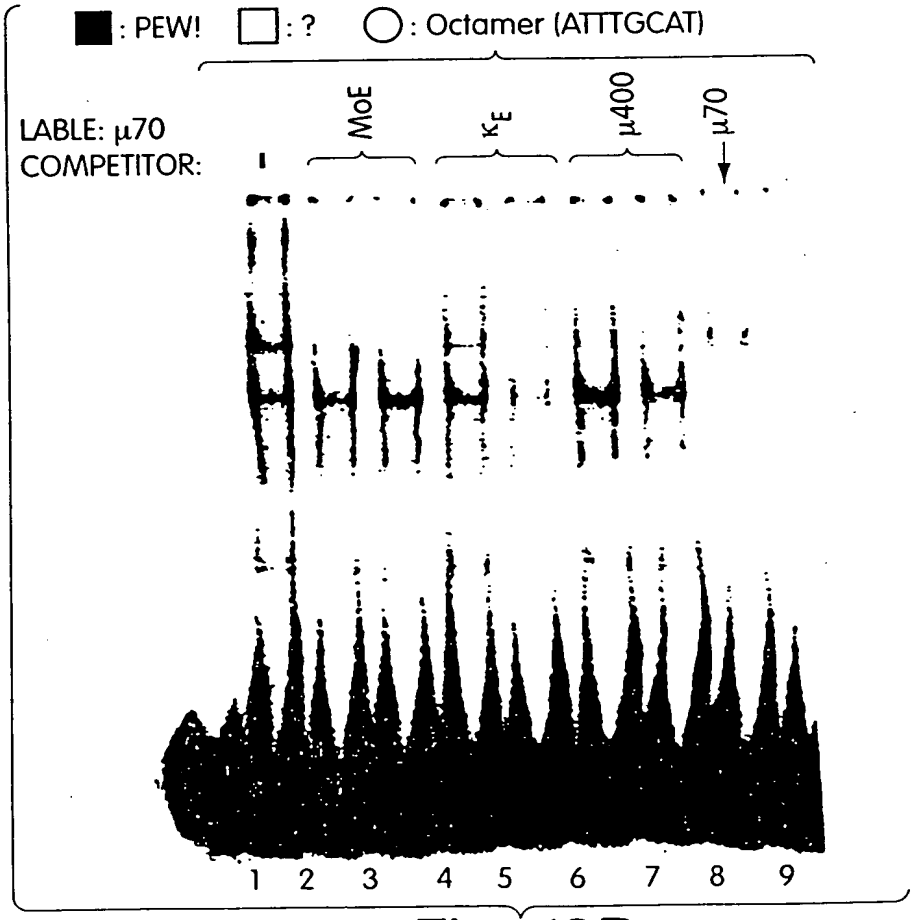


Fig. 10D

Figure 10E

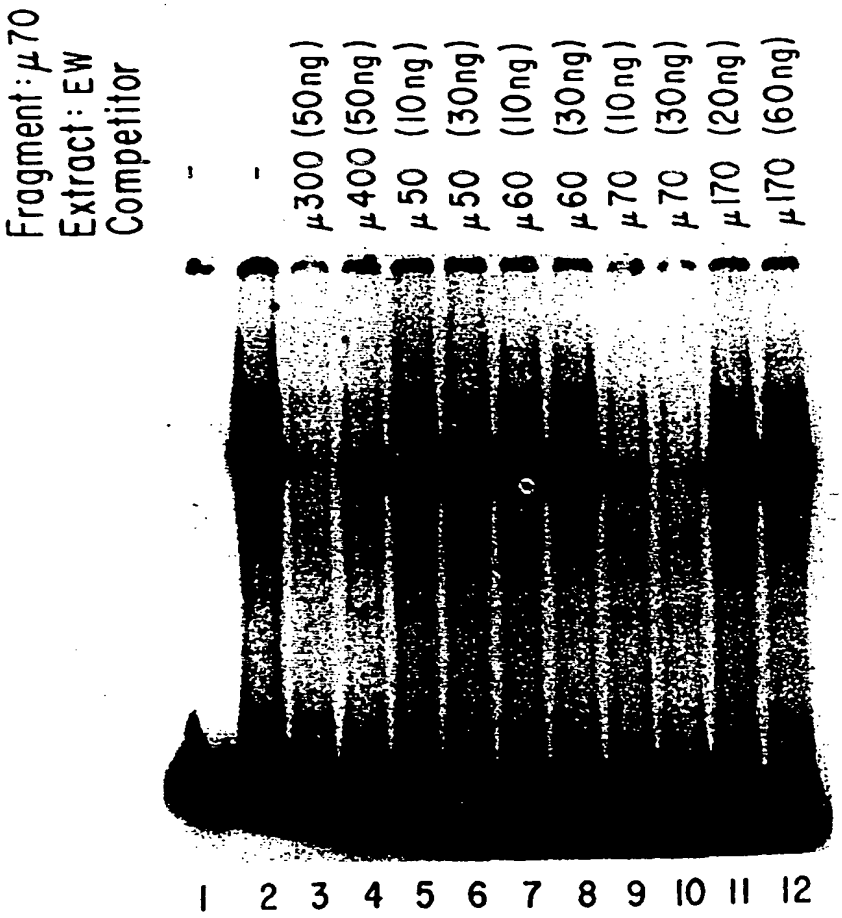
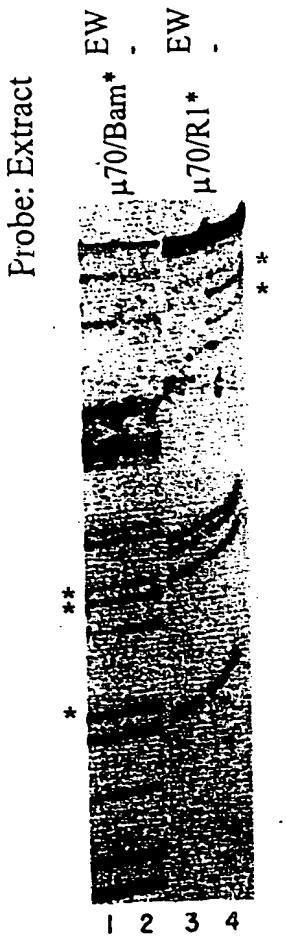

Fragment: μ70
Extract: EW
Competitor
-
-
μ300 (50ng)
μ400 (50ng)
μ50 (10ng)
μ50 (30ng)
μ60 (10ng)
μ60 (30ng)
μ70 (10ng)
μ70 (30ng)
μ170 (20ng)
μ170 (60ng)
1 2 3 4 5 6 7 8 9 10 11 12

Figure 11A

Figure 11B



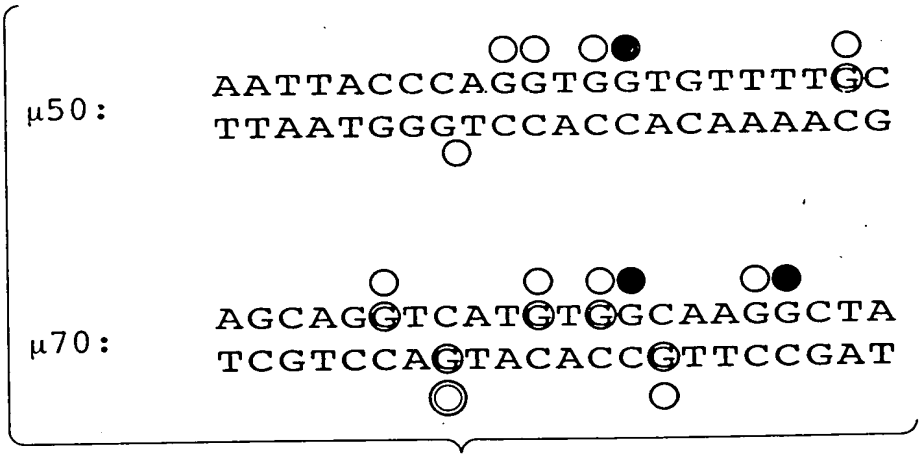

μ50:
AATTACCCAGGTGGTGTTTTGC
TTAATGGGTCCACCACAAAACG
μ70:
AGCAGGTCATGTGGCAAGGCTA
TCGTCCAGTACACCGTTCCGAT

Fig. 11C

Figure 12A

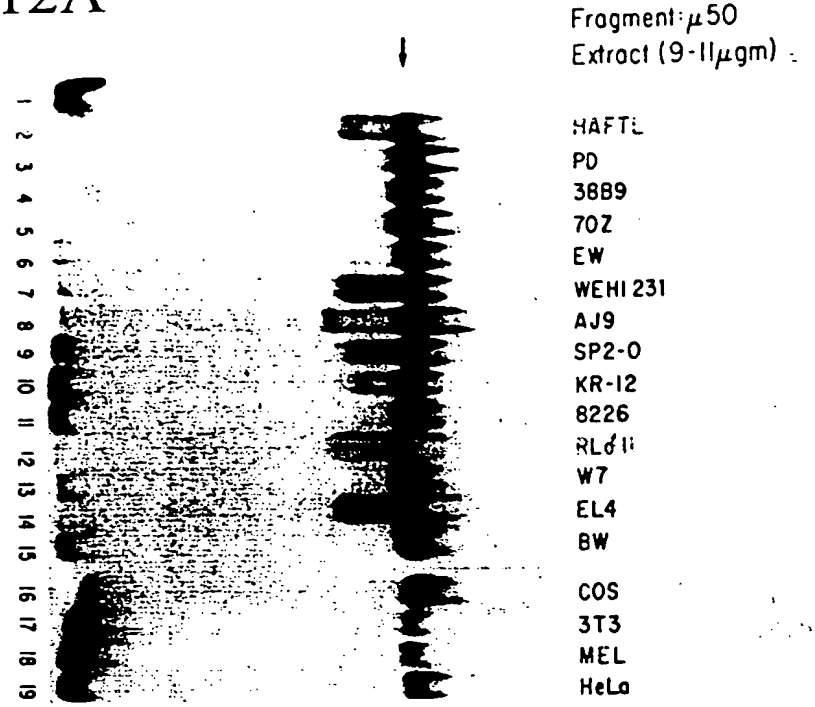


Figure 12B

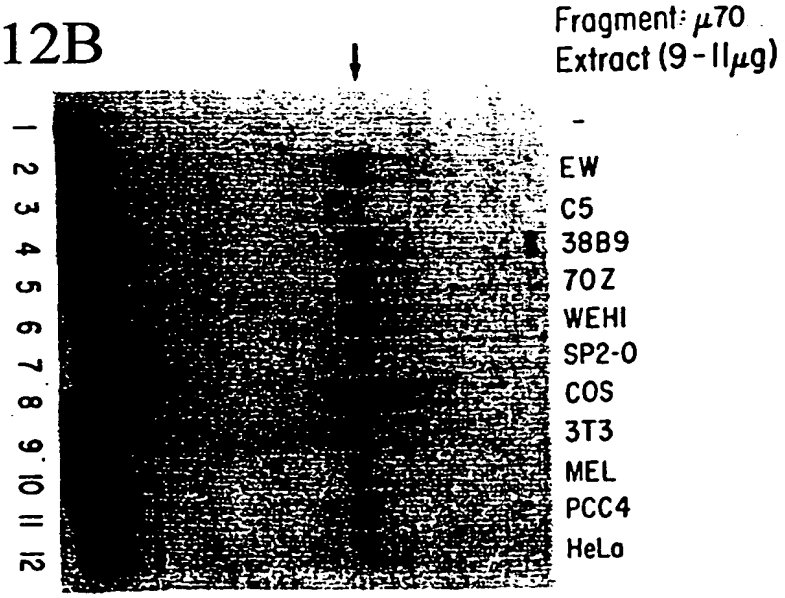


Figure 13A

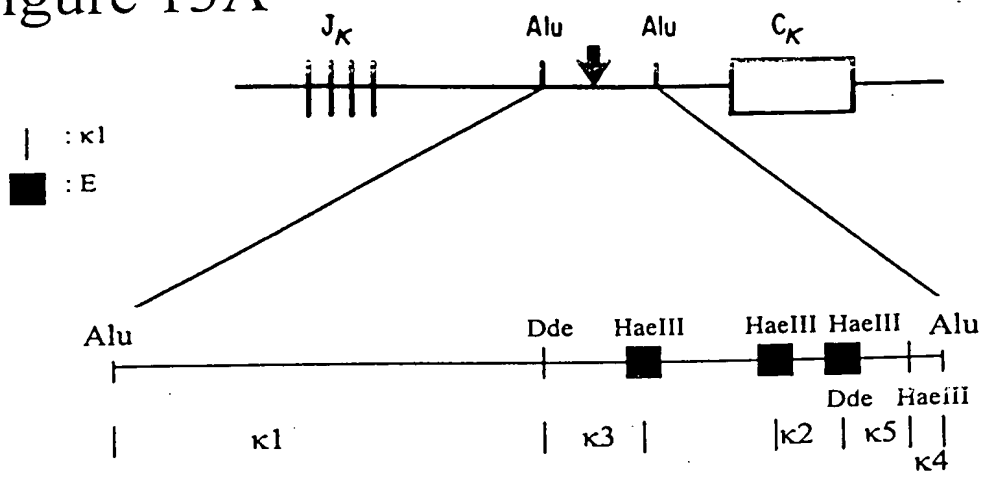


Figure 13B

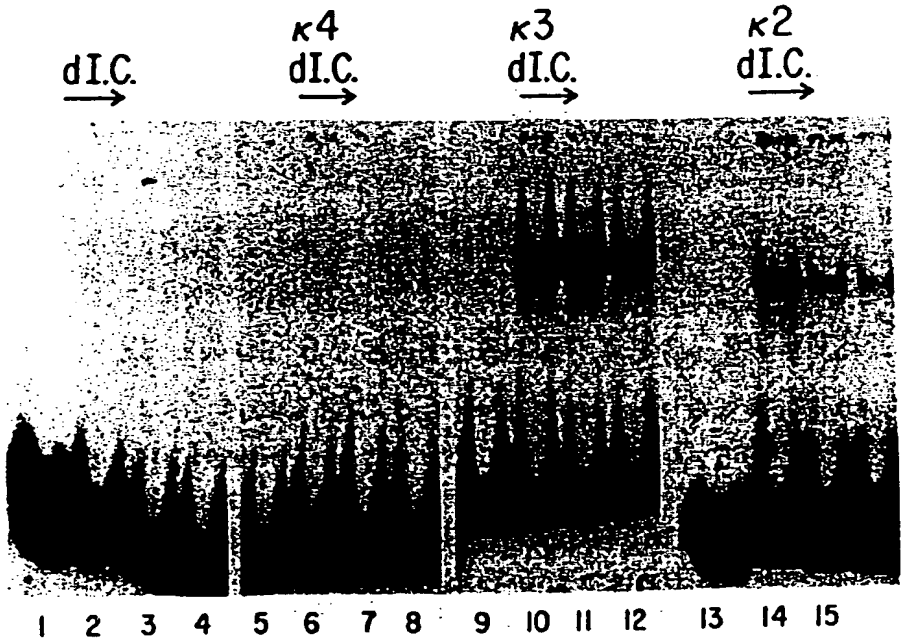


Figure 13C

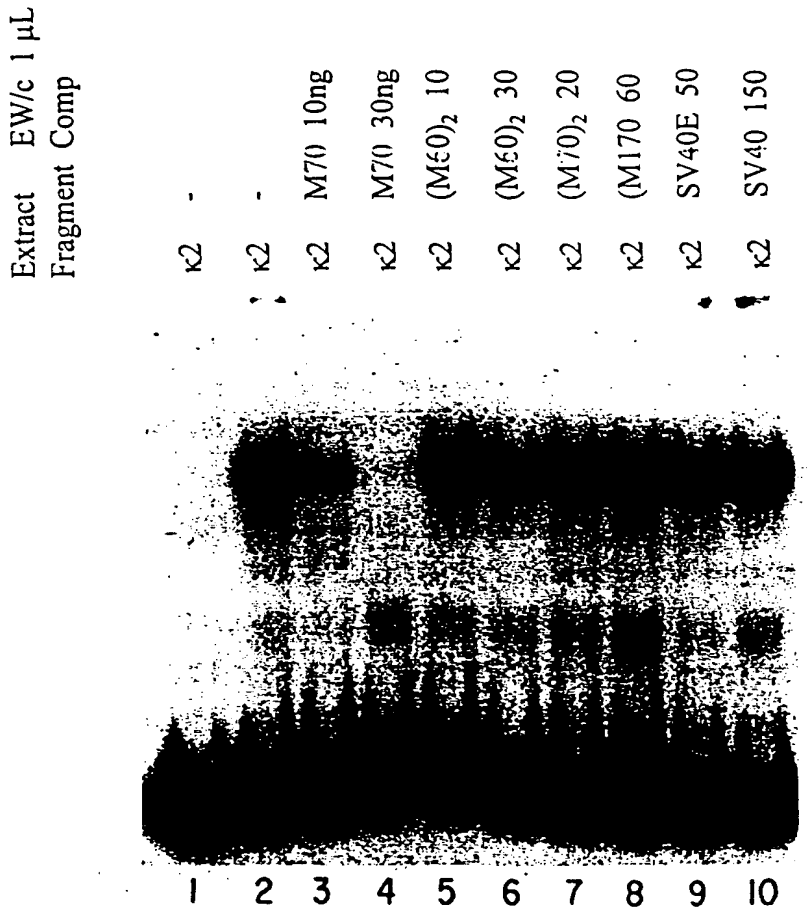

Extract EW/c 1 µL
Fragment Comp
κ2 -
κ2 -
κ2 M70 10ng
κ2 M70 30ng
κ2 (M60)2 10
κ2 (M60)2 30
κ2 (M70)2 20
κ2 (M170 60
κ2 SV40E 50
κ2 SV40 150
1 2 3 4 5 6 7 8 9 10

Figure 13D

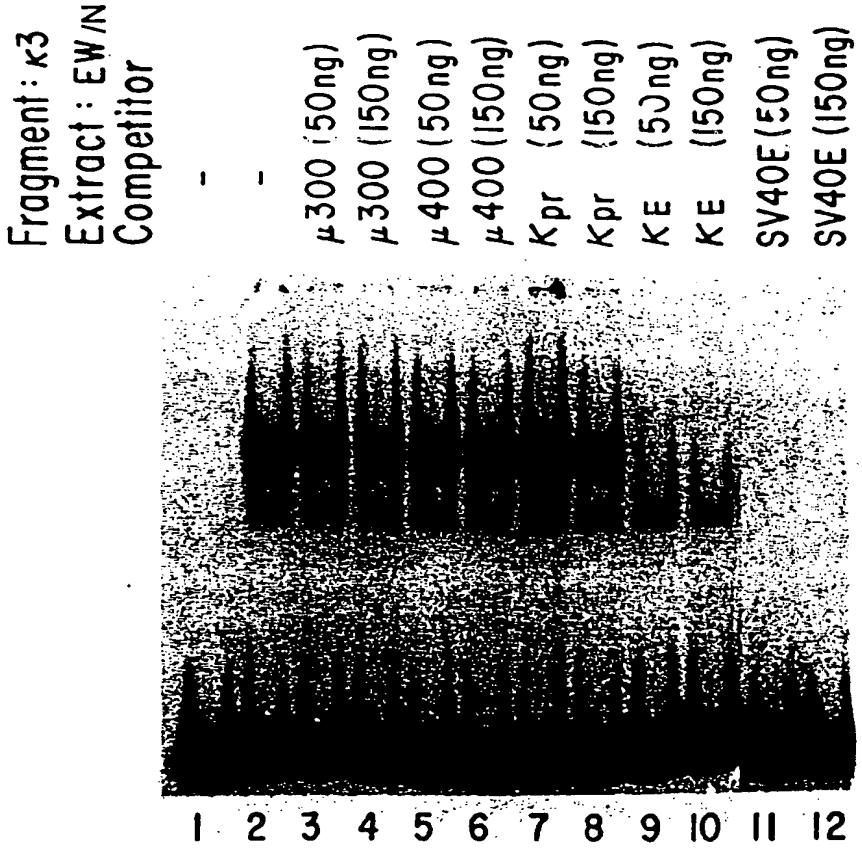

Fragment: κ3
Extract: EW/N
Competitor
-
-
μ300 (50ng)
μ300 (150ng)
μ400 (50ng)
μ400 (150ng)
Kpr (50ng)
Kpr (150ng)
KE (50ng)
KE (150ng)
SV40E (50ng)
SV40E (150ng)
1 2 3 4 5 6 7 8 9 10 11 12

Figure 14

Figure 15A

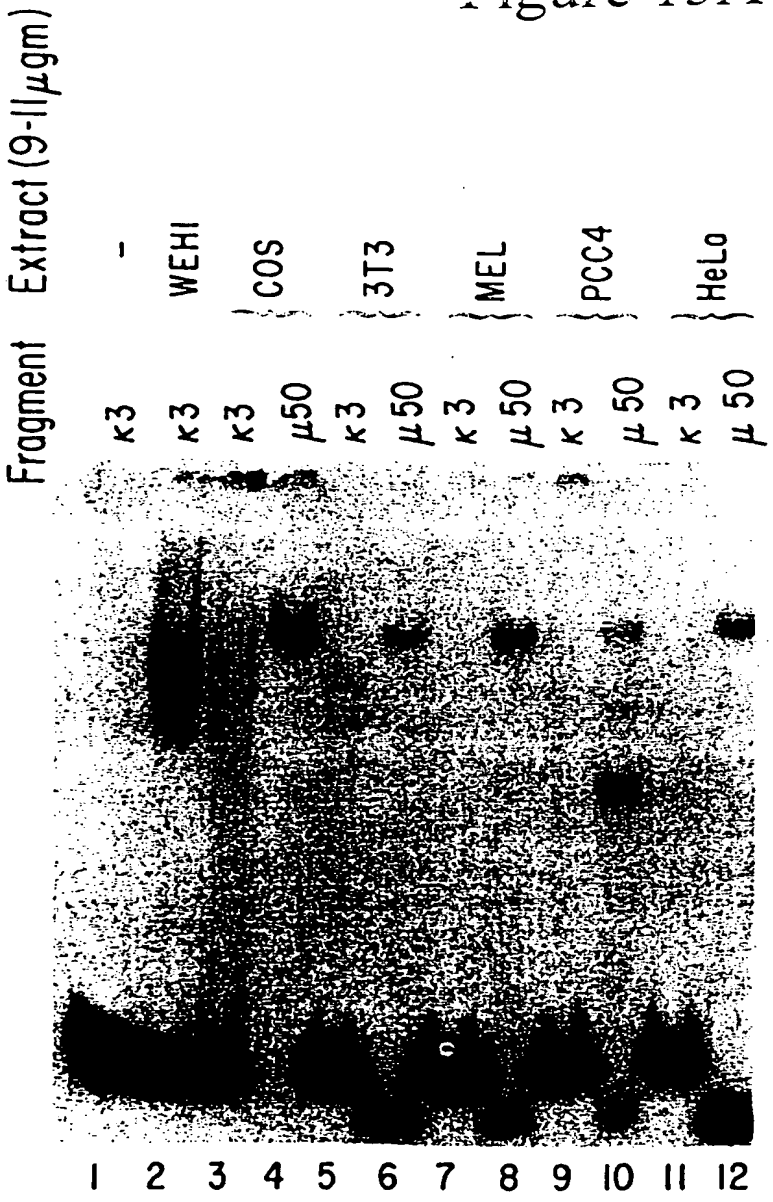
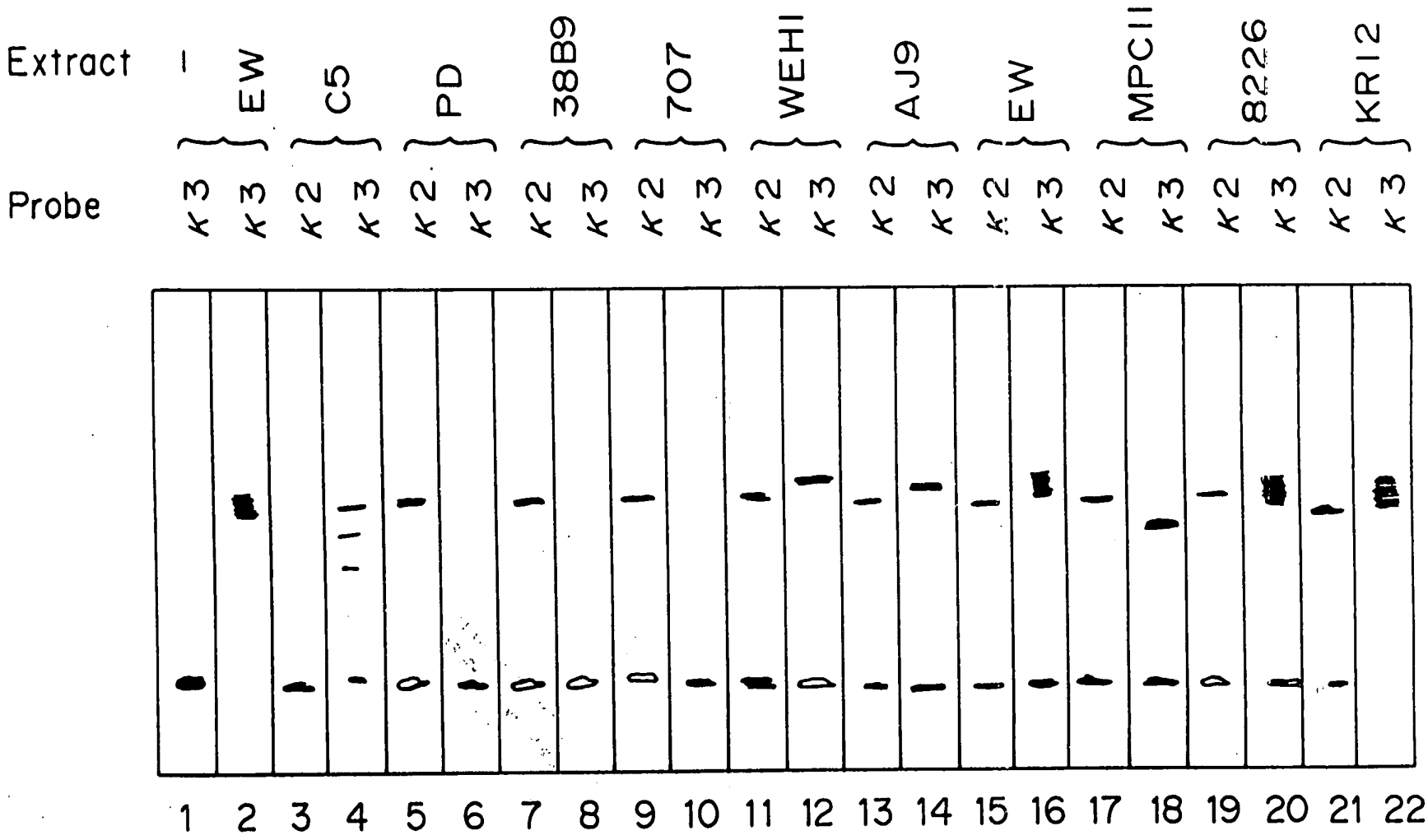

Fragment
Extract (9-11μgm)
-
WEHI
COS
3T3
MEL
PCC4
HeLa
κ3
κ3
κ3
μ50
κ3
μ50
κ3
μ50
κ3
μ50
κ3
μ50
1 2 3 4 5 6 7 8 9 10 11 12

FIGURE 15b


Extract
-
EW
C5
PD
38B9
707
WEHI
AJ9
EW
MPCII
8226
KR12
Probe
κ3 κ3 κ2 κ3 κ2 κ3 κ2 κ3 κ2 κ3 κ2 κ3 κ2 κ3 κ2 κ3 κ2 κ3 κ2 κ3 κ2 κ3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22

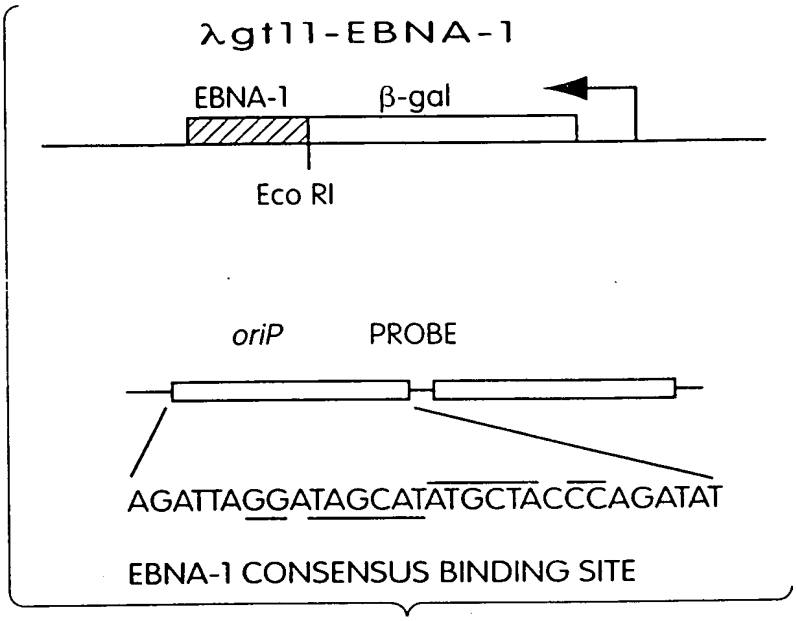


Fig. 16

MHC	TGGGGATTCCCCA
mhc1	TGcGGATTCCCaA
κ EN	aGGGGACTttCCg
κ en	aaattAcTttCCg
SVEN	TGGGGAcTttCCA
HIV	TGGGGAcTttCCA
	aaGGGAcTttCCg

Fig. 17

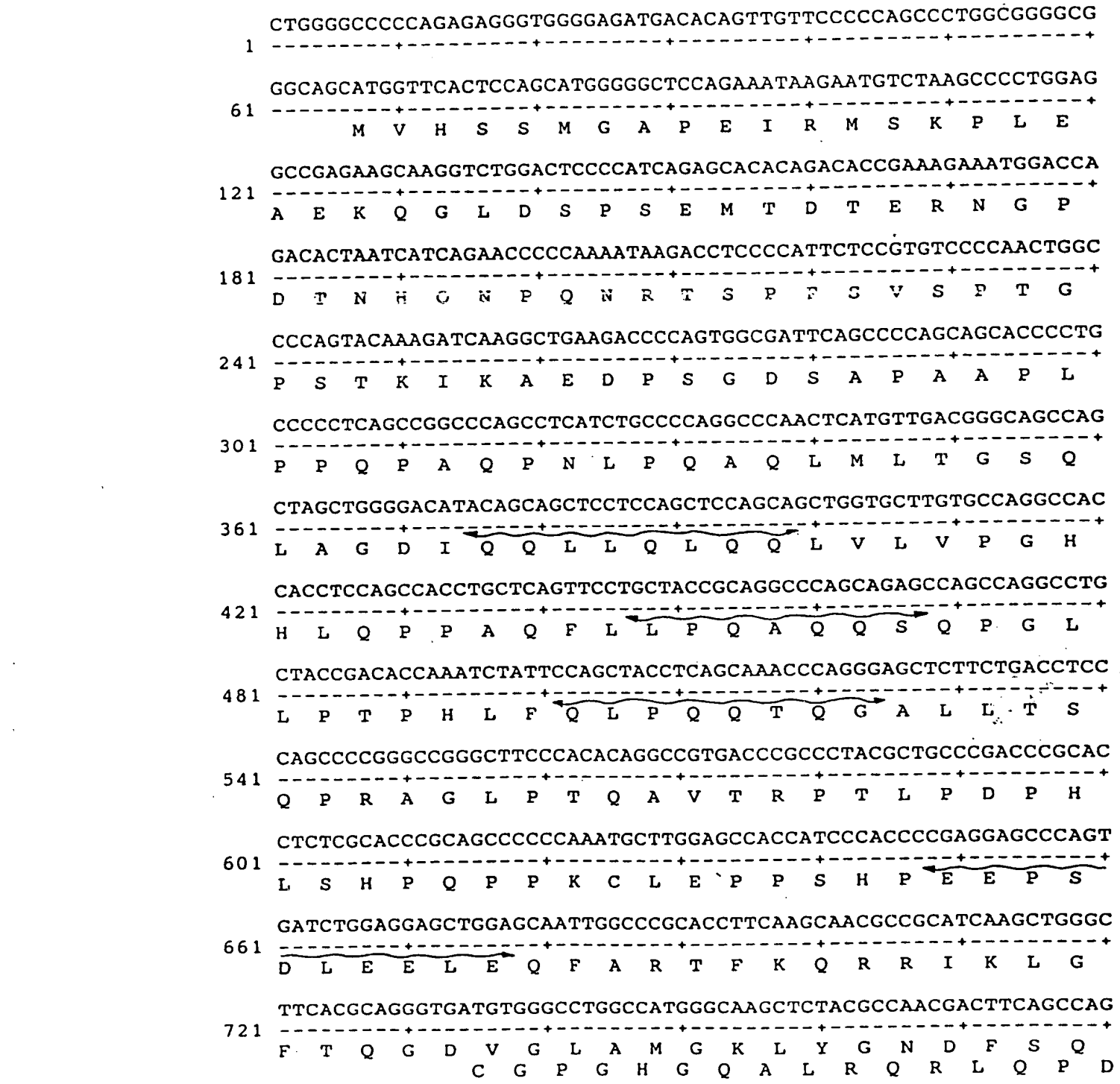

CTGGGGCCCCCAGAGAGGGTGGGGAGATGACACAGTTGTTCCCCCAGCCCTGGCGGGGCG
1
GGCAGCATGGTTCACTCCAGCATGGGGGCTCCAGAAATAAGAATGTCTAAGCCCCTGGAG
61
M V H S S M G A P E I R M S K P L E
GCCGAGAAGCAAGGTCTGGACTCCCCATCAGAGCACACAGACACCGAAAGAAATGGACCA
121
A E K Q G L D S P S E M T D T E R N G P
GACACTAATCATCAGAACCCCCAAAATAAGACCTCCCCATTCTCCGTGTCCCCAACTGGC
181
D T N H Q N P Q N R T S P F S V S P T G
CCCAGTACAAAGATCAAGGCTGAAGACCCCAGTGGCGATTCAGCCCCAGCAGCACCCCTG
241
P S T K I K A E D P S G D S A P A A P L
CCCCCTCAGCCGGCCCAGCCTCATCTGCCCCAGGCCCAACTCATGTTGACGGGCAGCCAG
301
P P Q P A Q P N L P Q A Q L M L T G S Q
CTAGCTGGGGACATACAGCAGCTCCTCCAGCTCCAGCAGCTGGTGCTTGTGCCAGGCCAC
361
L A G D I Q Q L L Q L Q Q L V L V P G H
CACCTCCAGCCACCTGCTCAGTTCCTGCTACCGCAGGCCCAGCAGAGCCAGCCAGGCCTG
421
H L Q P P A Q F L L P Q A Q Q S Q P G L
CTACCGACACCAAATCTATTCCAGCTACCTCAGCAAACCCAGGGAGCTCTTCTGACCTCC
481
L P T P H L F Q L P Q Q T Q G A L L T S
CAGCCCCGGGCCGGGCTTCCCACACAGGCCGTGACCCGCCCTACGCTGCCCGACCCGCAC
541
Q P R A G L P T Q A V T R P T L P D P H
CTCTCGCACCCGCAGCCCCCCAAATGCTTGGAGCCACCATCCCACCCCGAGGAGCCCAGT
601
L S H P Q P P K C L E P P S H P E E P S
GATCTGGAGGAGCTGGAGCAATTGGCCCGCACCTTCAAGCAACGCCGCATCAAGCTGGGC
661
D L E E L E Q F A R T F K Q R R I K L G
TTCACGCAGGGTGATGTGGGCCTGGCCATGGGCAAGCTCTACGCCAACGACTTCAGCCAG
721
F T Q G D V G L A M G K L Y G N D F S Q
C G P G H G Q A L R Q R L Q P D

Fig. 18A

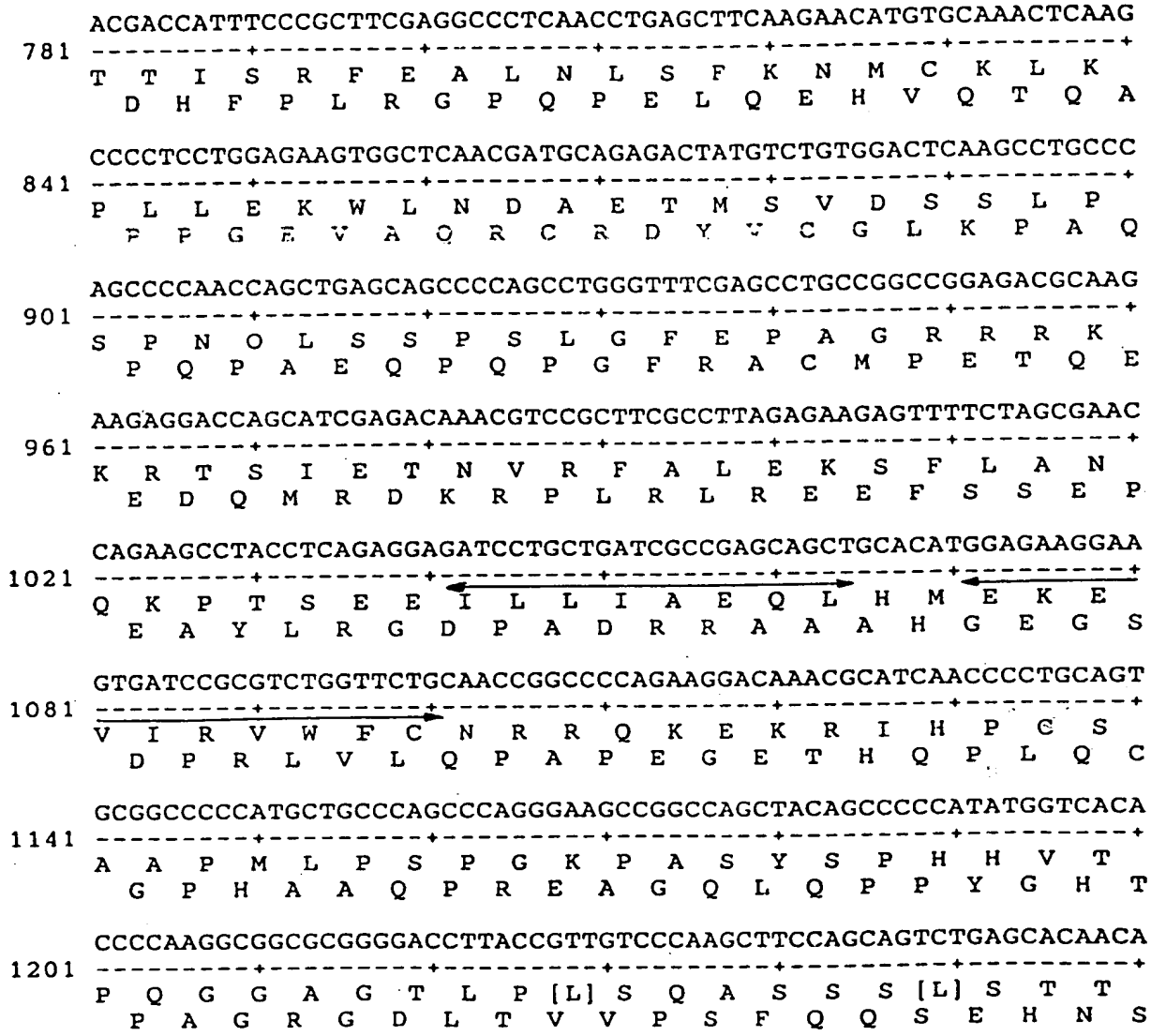


Fig. 18A
(CONTINUED)

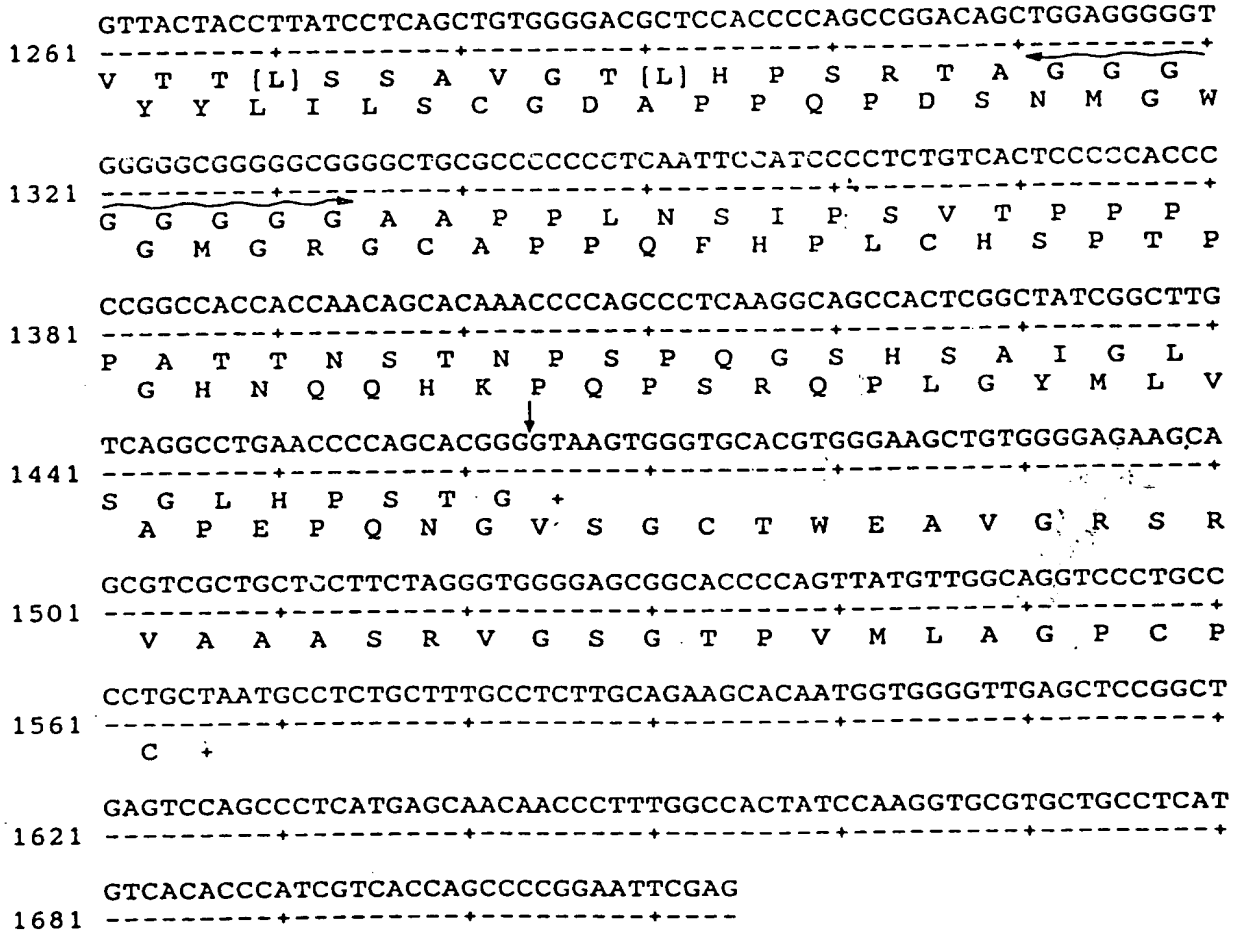


Fig. 18A
(CONTINUED)

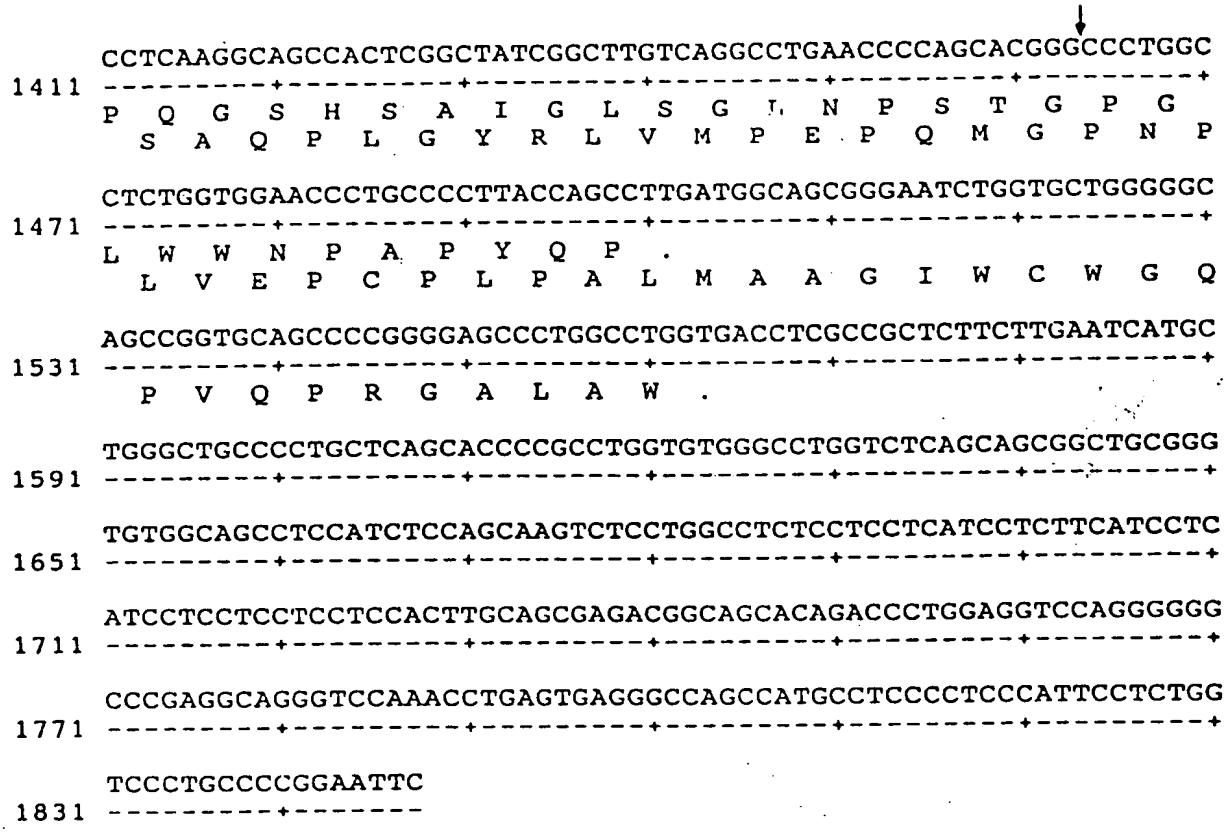

CCTCAAGGCAGCCACTCGGCTATCGGCTTGTCAGGCCTGAACCCCAGCACGGGCCCTGGC
1411
P Q G S H S A I G L S G L N P S T G P G
S A Q P L G Y R L V M P E P Q M G P N P
CTCTGGTGGAACCCTGCCCCTTACCAGCCTTGATGGCAGCGGGAATCTGGTGCTGGGGGC
1471
L W W N P A P Y Q P .
L V E P C P L P A L M A A G I W C W G Q
AGCCGGTGCAGCCCCGGGGAGCCCTGGCCTGGTGACCTCGCCGCTCTTCTTGAATCATGC
1531
P V Q P R G A L A W .
TGGGCTGCCCCTGCTCAGCACCCCGCCTGGTGTGGGCCTGGTCTCAGCAGCGGCTGCGGG
1591
TGTGGCAGCCTCCATCTCCAGCAAGTCTCCTGGCCTCTCCTCCTCATCCTCTTCATCCTC
1651
ATCCTCCTCCTCCTCCACTTGCAGCGAGACGGCAGCACAGACCCTGGAGGTCCAGGGGGG
1711
CCCGAGGCAGGGTCCAAACCTGAGTGAGGGCCAGCCATGCCTCCCCTCCCATTCCTCTGG
1771
TCCCTGCCCCGGAATTC
1831

Fig. 18B

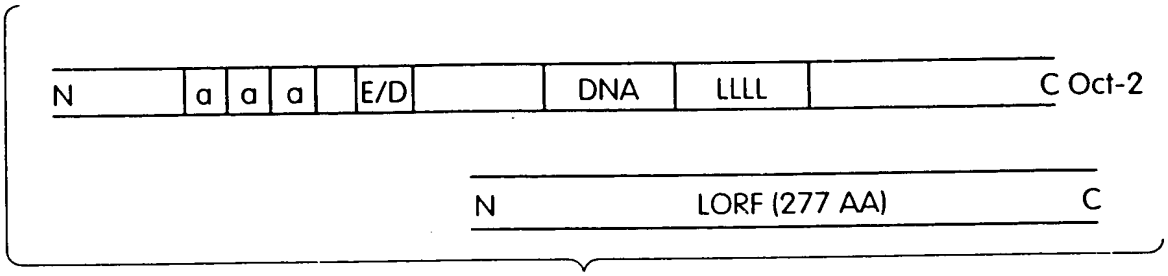


Fig. 18C

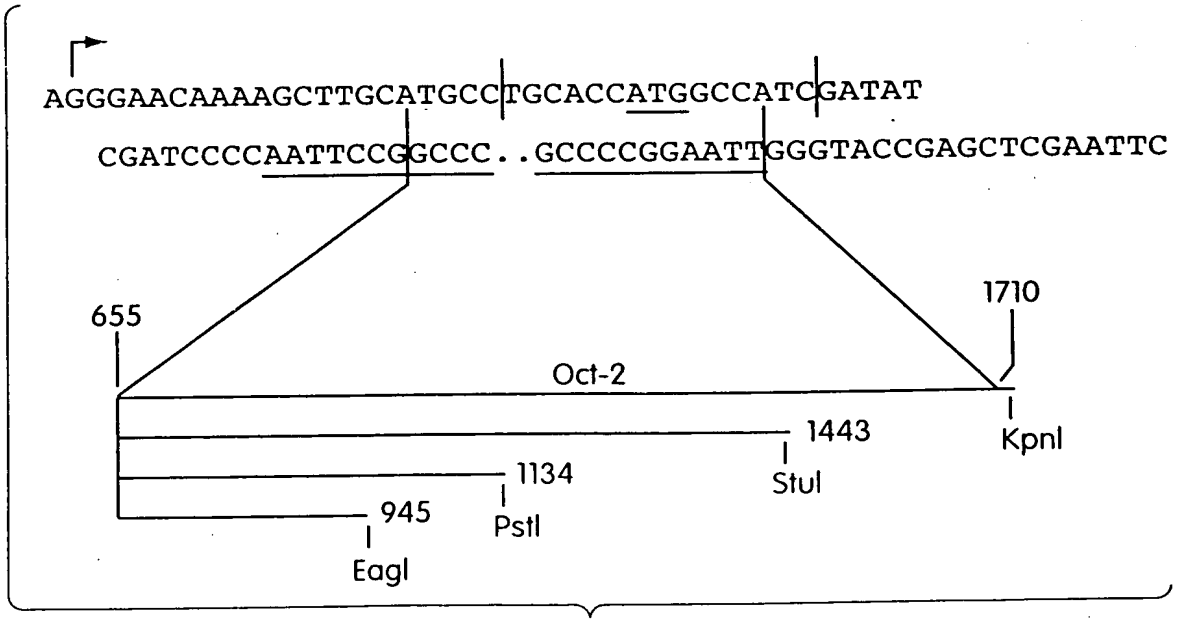


Fig. 19

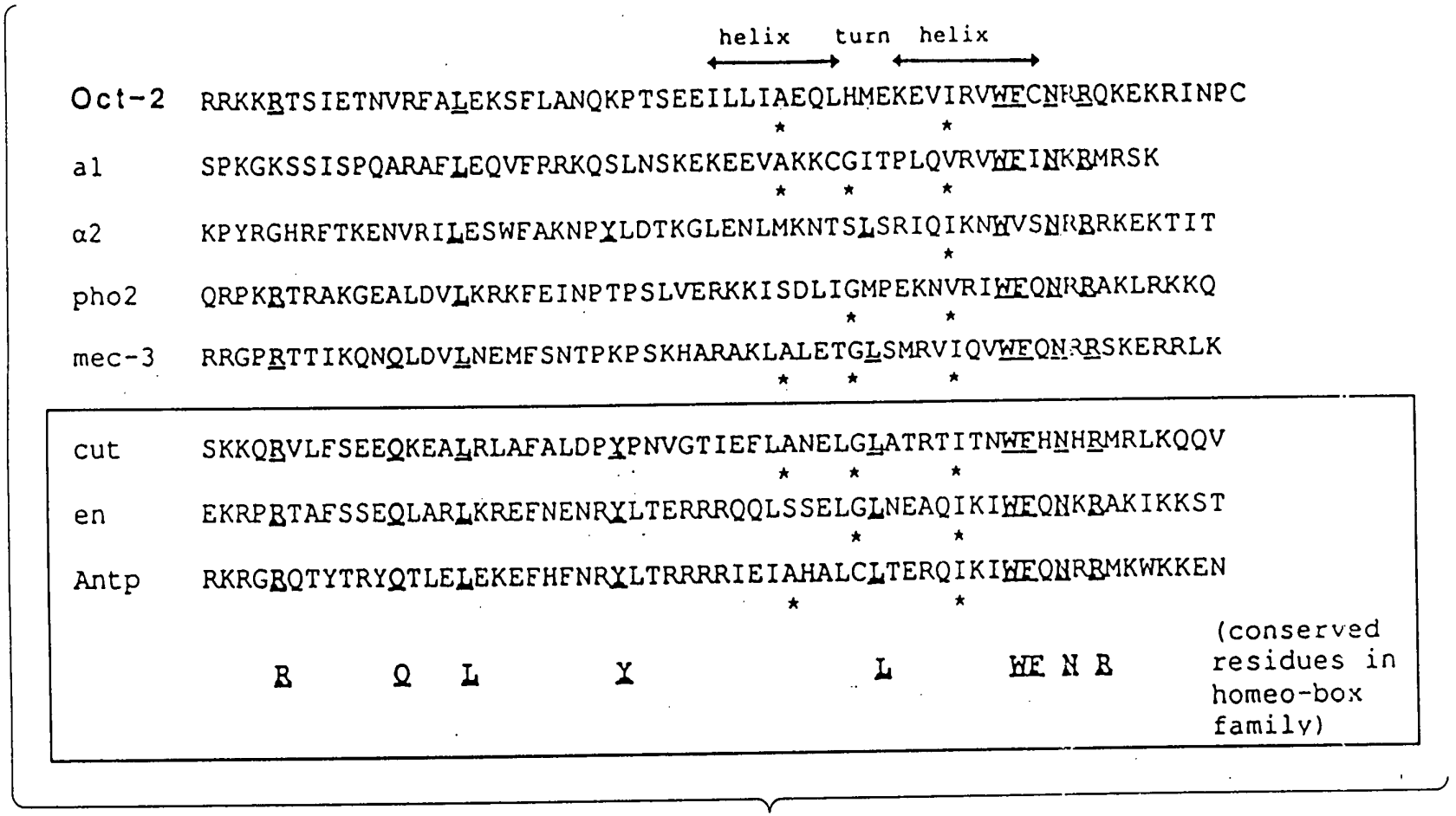

helix
turn
helix
Oct-2 RRKKRTSIETNVRFALEKSFLANQKPTSEEILLIAEQLHMEKEVIRVWFCNRRQKEKRINPC
a1 SPKGKSSISPQARAFLEQVFRRKQSLNSKEKEEVAKKCGITPLQVRVWFINKRMRSK
α2 KPYRGHRFTKENVRILESWFAKNPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKTIT
pho2 QRPKRTRAKGEALDVLKRKFEINPTPSLVERKKISDLIGMPEKNVRIWFQNRRAKLRKKQ
mec-3 RRGPRTTIKQNQLDVLNEMFSNTPKPSKHARAKLALETGLSMRVIQVWFQNRRSKERRLK
cut SKKQRVLFSEEQKEALRLAFALDPYPNVGTIEFLANELGLATRTITNWFHNHRMRLKQQV
en EKRPRTAFSSEQLARLKREFNENRYLTERRRQQLSSELGLNEAQIKIWFQNKRAKIKKST
Antp RKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKEN
R Q L Y L WF N R
(conserved residues in homeo-box family)

Fig. 20

Figure 21A

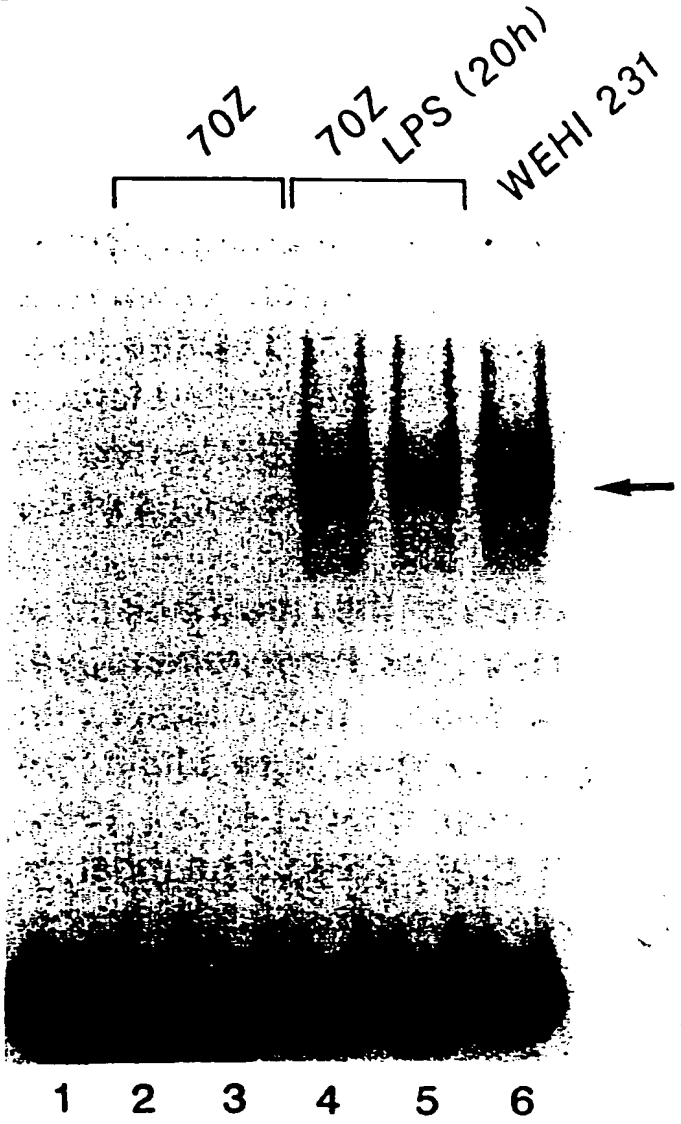


Figure 21B

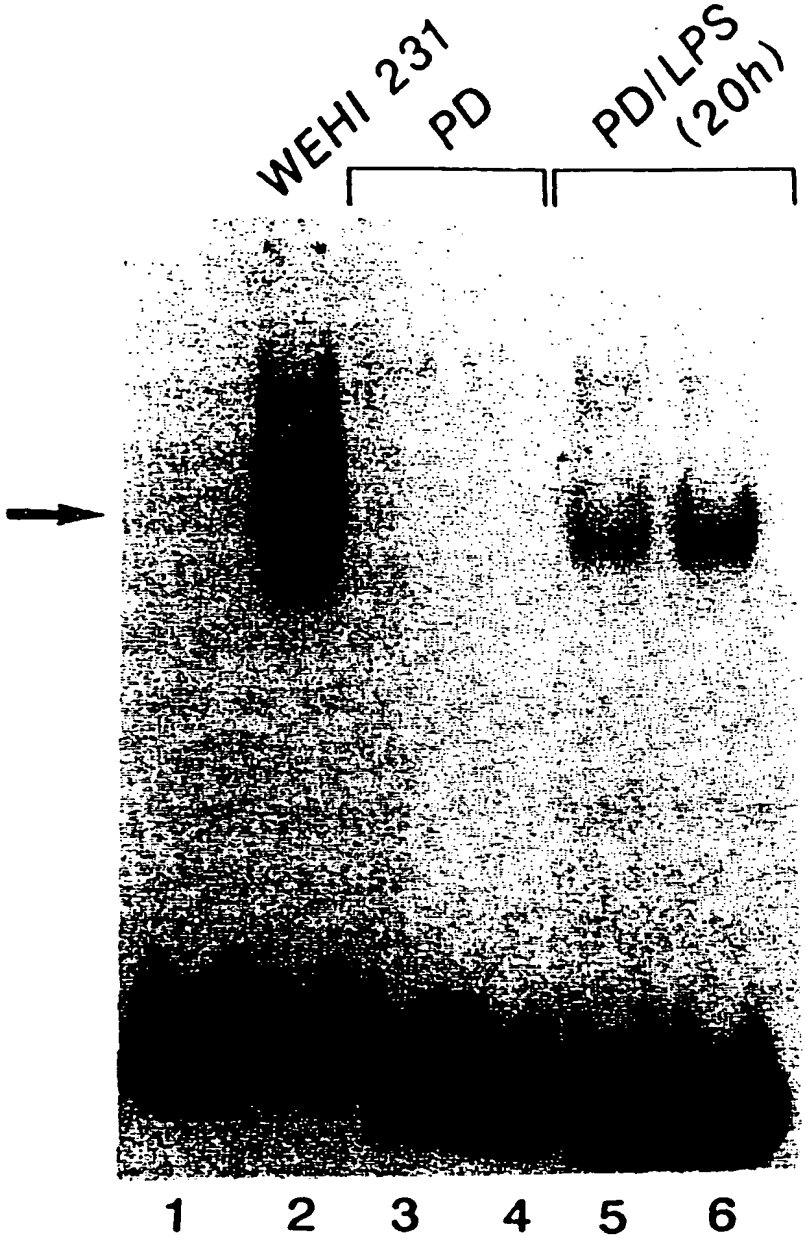


Figure 22A

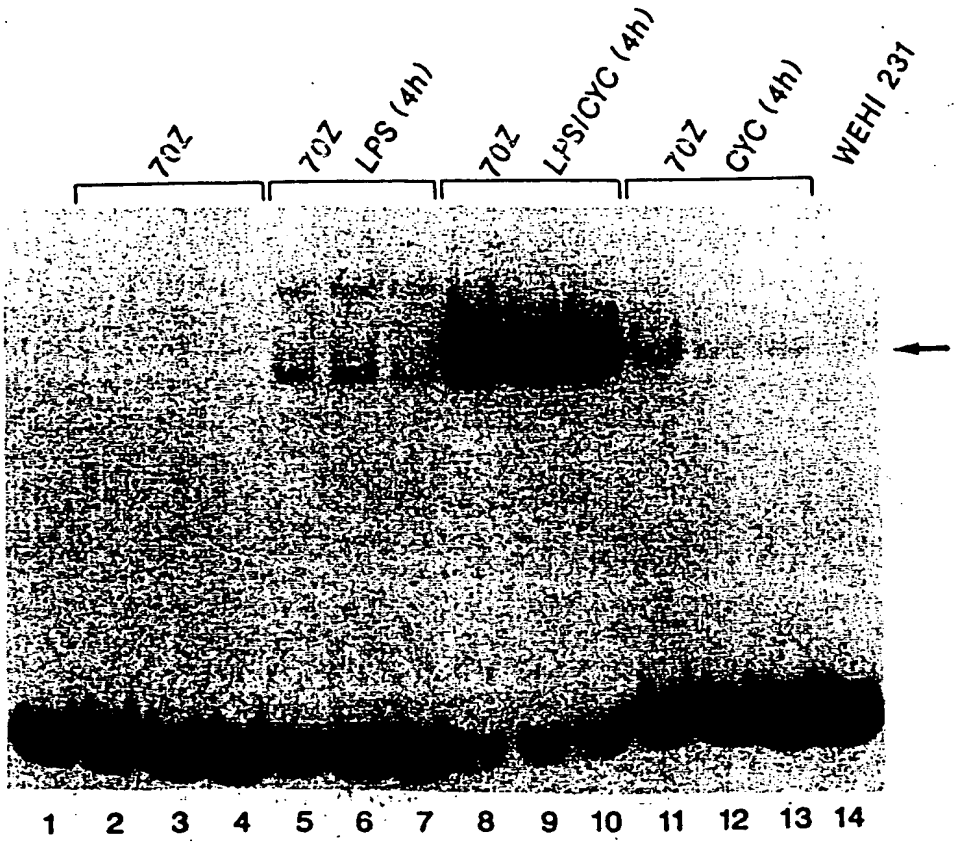

70Z
70Z LPS (4h)
70Z LPS/CYC (4h)
70Z CYC (4h)
WEHI 231
1 2 3 4 5 6 7 8 9 10 11 12 13 14

Figure 22B

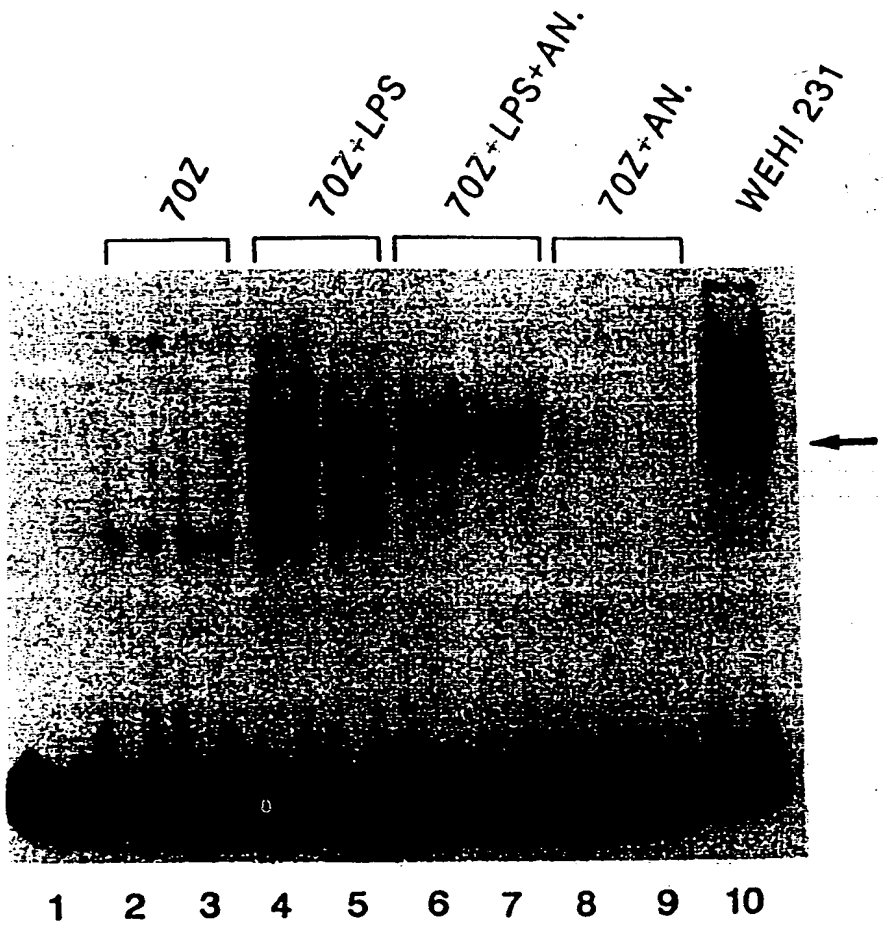


Figure 23A

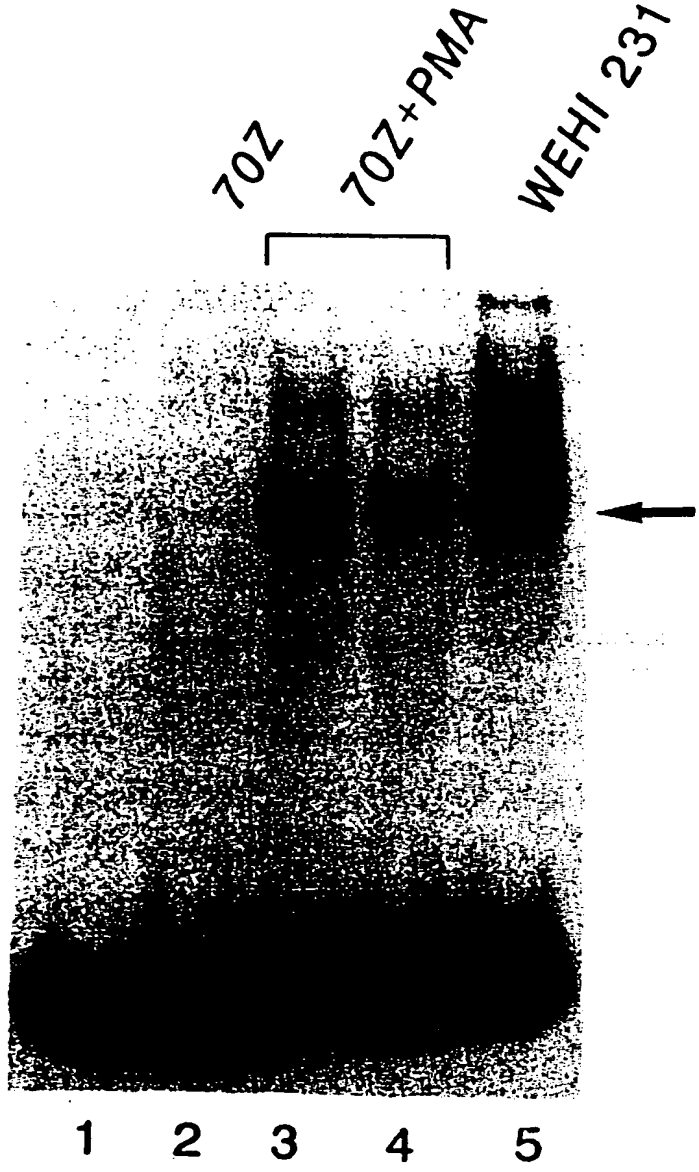


Figure 23B

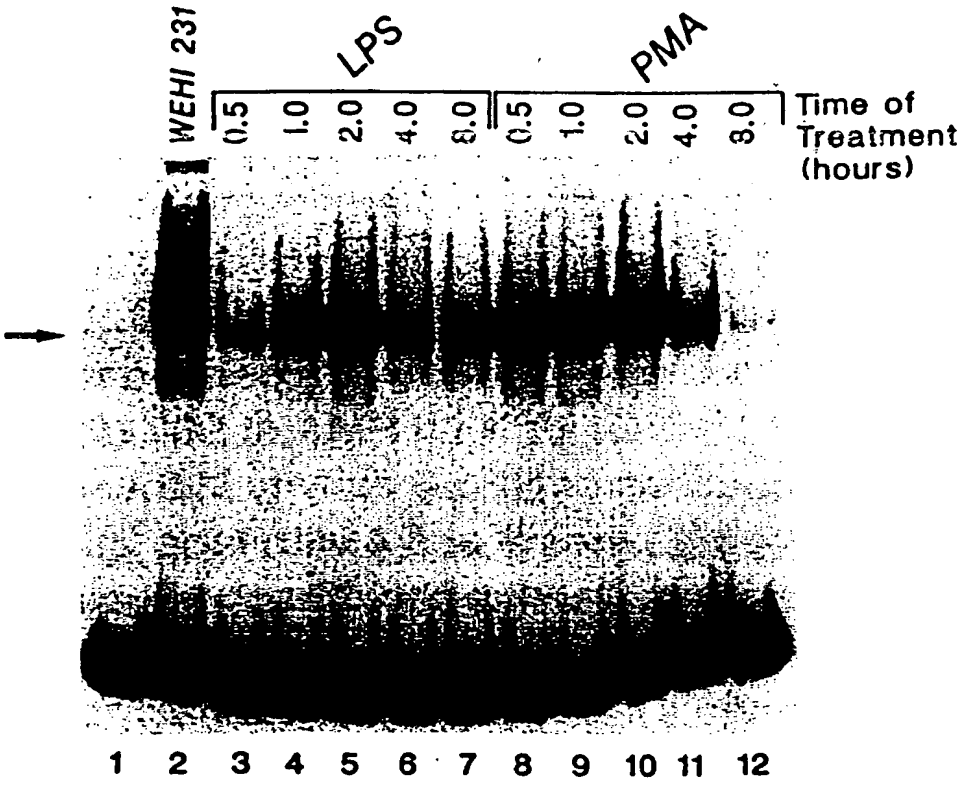

WEHI 231
LPS
PMA
0.5
1.0
2.0
4.0
8.0
0.5
1.0
2.0
4.0
8.0
Time of Treatment (hours)
1 2 3 4 5 6 7 8 9 10 11 12

Figure 24A

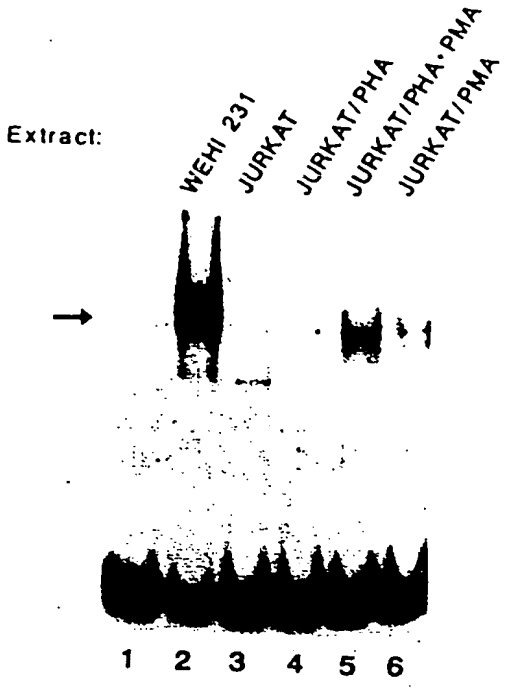


Figure 24B

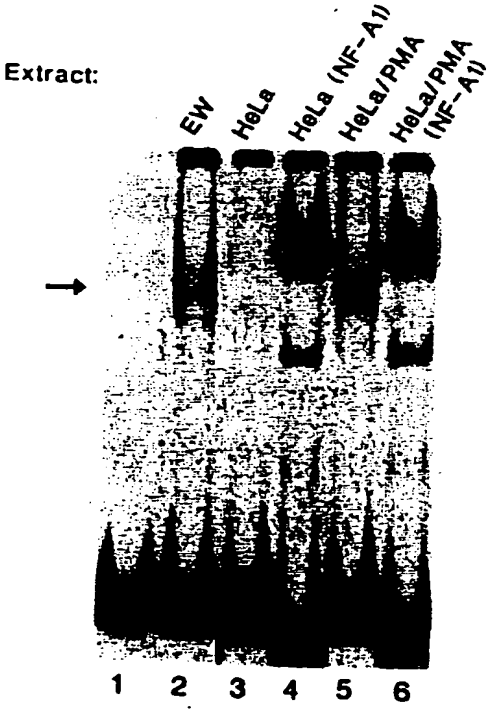
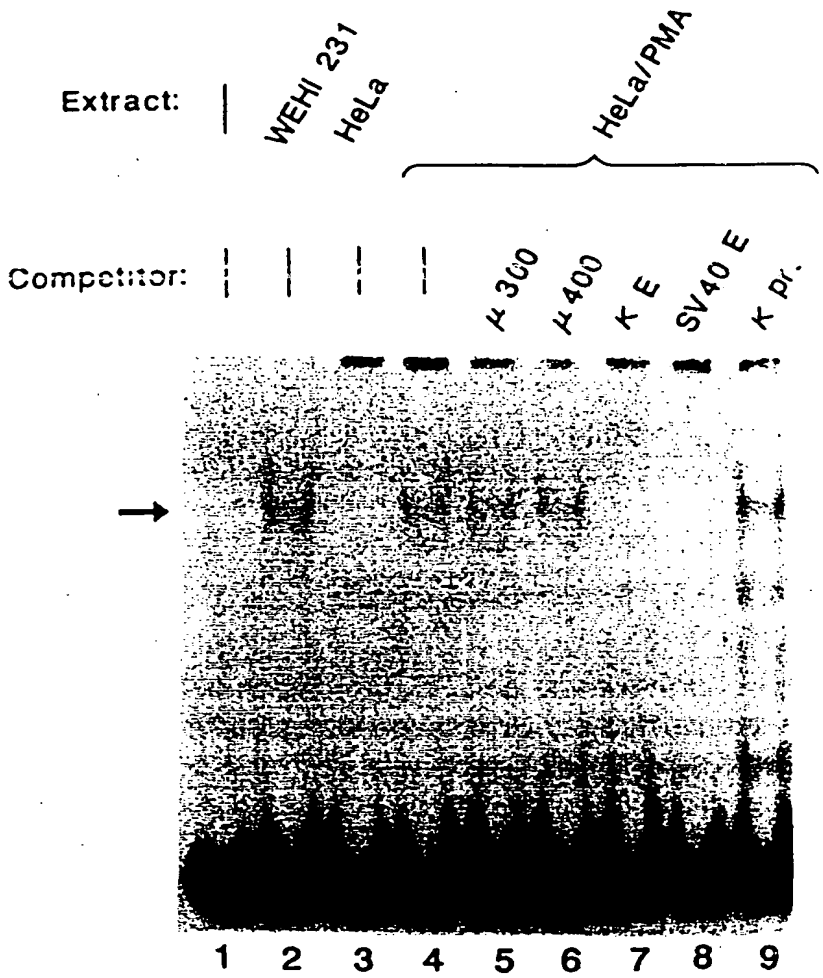


Figure 24C


Extract:
WEHI 231
HeLa
HeLa/PMA
Competitor:
μ 300
μ 400
κ E
SV40 E
κ pr.
1 2 3 4 5 6 7 8 9

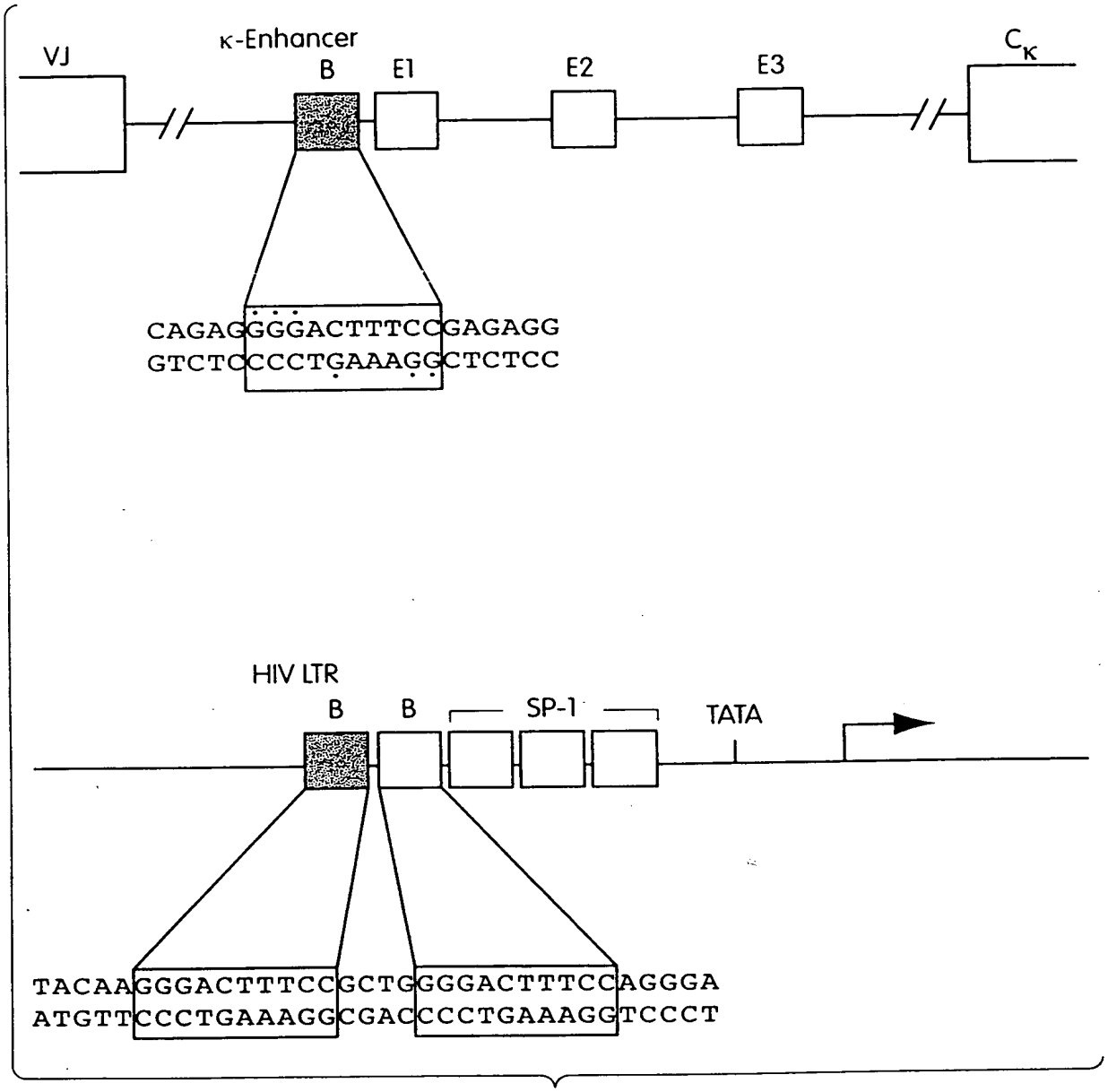

VJ
κ-Enhancer
B
E1
E2
E3
C_κ
CAGAGGGGACTTTCCGAGAGG
GTCTCCCCTGAAAGGCTCTCC
HIV LTR
B
B
SP-1
TATA
TACAAGGGACTTTCCGCTGGGGACTTTCCAGGGA
ATGTTCCCTGAAAGGCGACCCCTGAAAGGTCCCT

Fig. 25

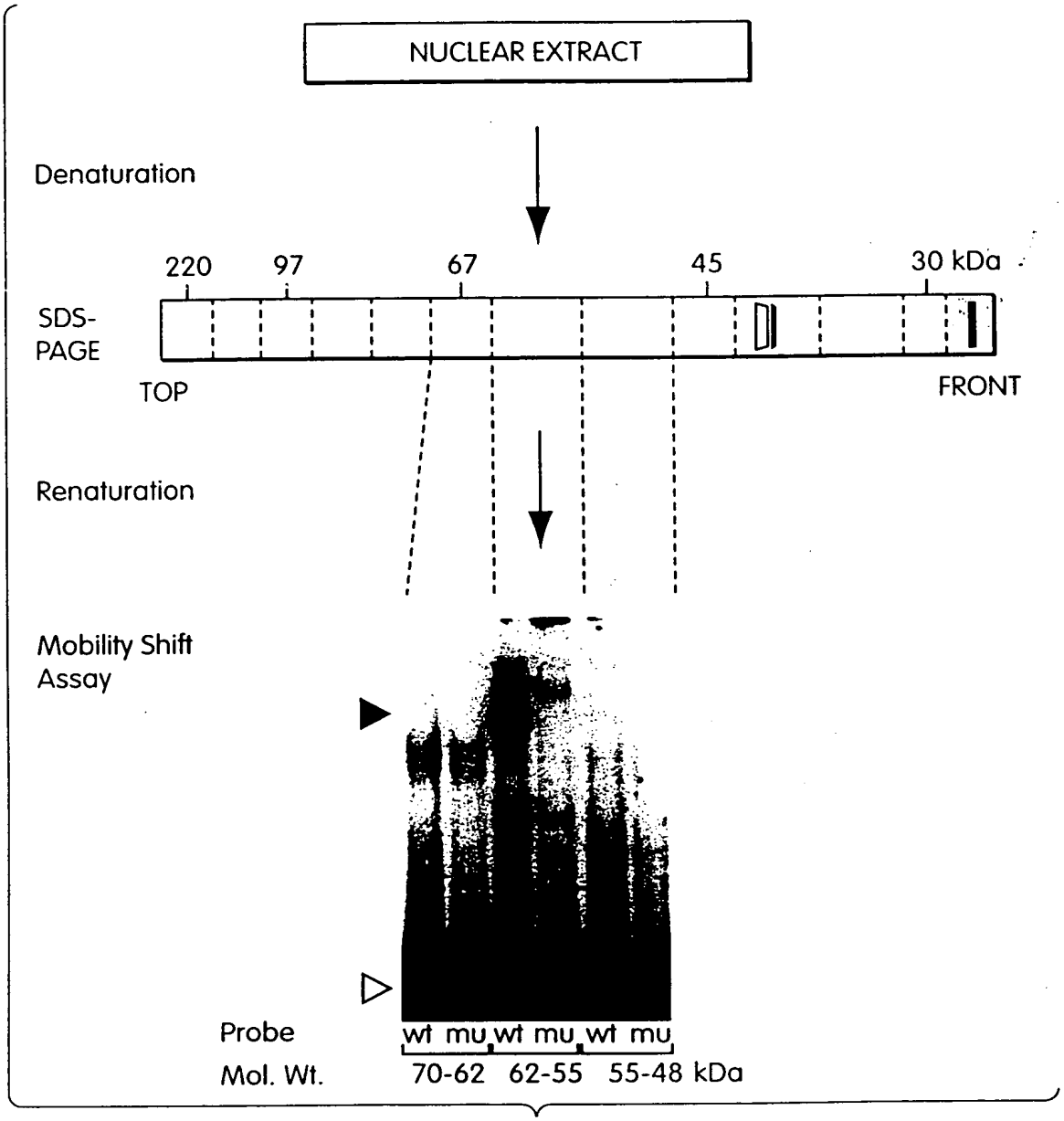

NUCLEAR EXTRACT
Denaturation
220
97
67
45
30 kDa
SDS-
PAGE
TOP
FRONT
Renaturation
Mobility Shift
Assay
Probe
wt mu wt mu wt mu
Mol. Wt.
70-62 62-55 55-48 kDa

Fig. 26A

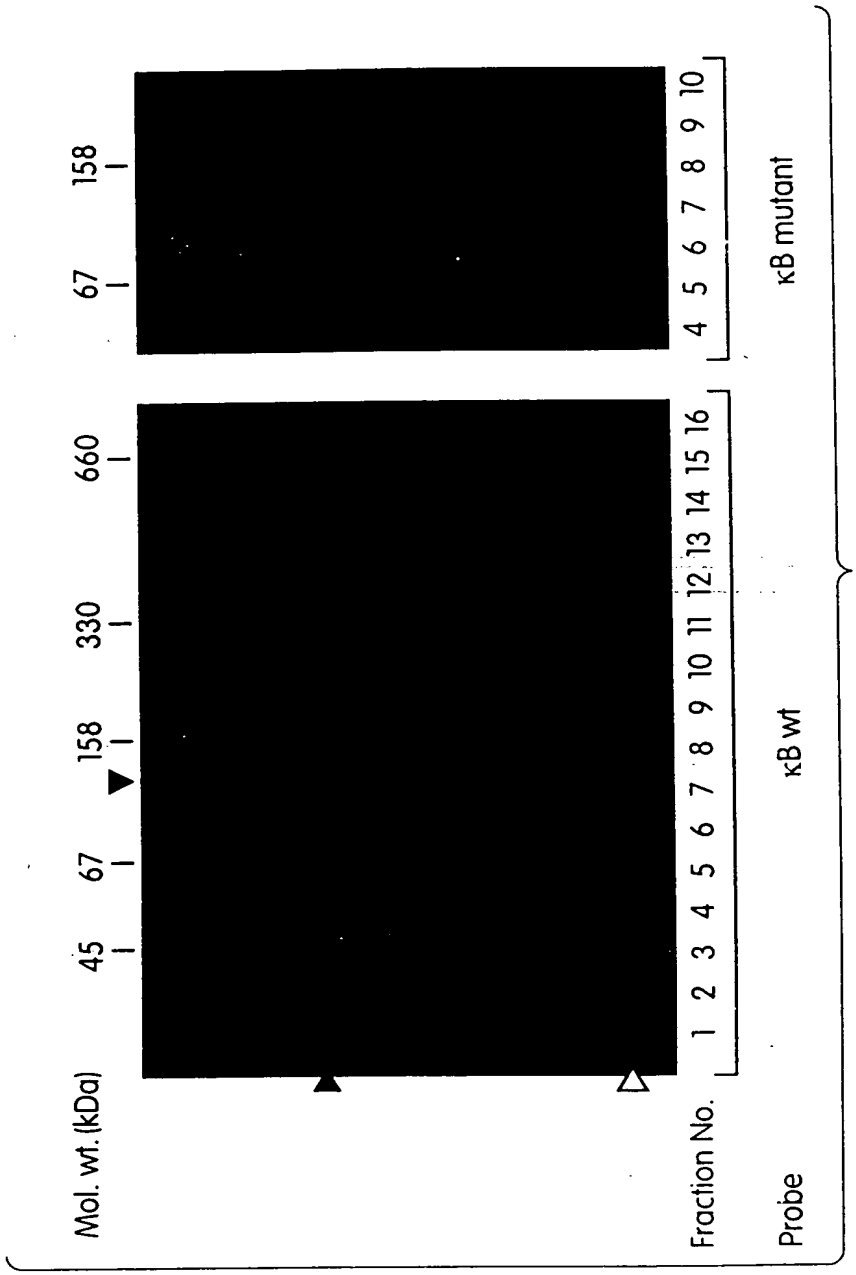

Mol. wt. (kDa)
45
67
158
330
660
Fraction No.
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
Probe
κB wt
67
158
4 5 6 7 8 9 10
κB mutant

Fig. 26B

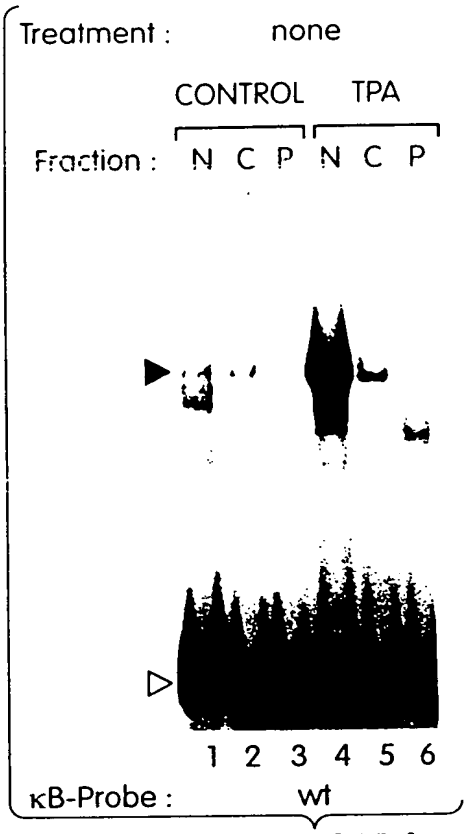


Fig. 27A

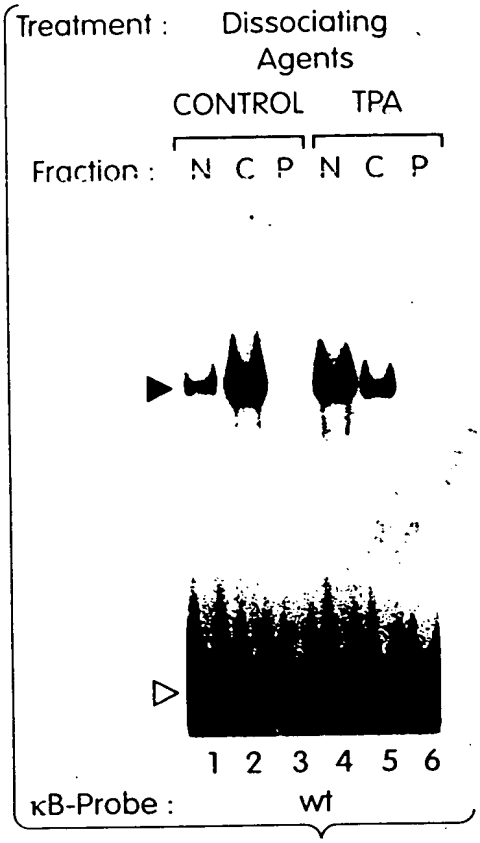


Fig. 27B

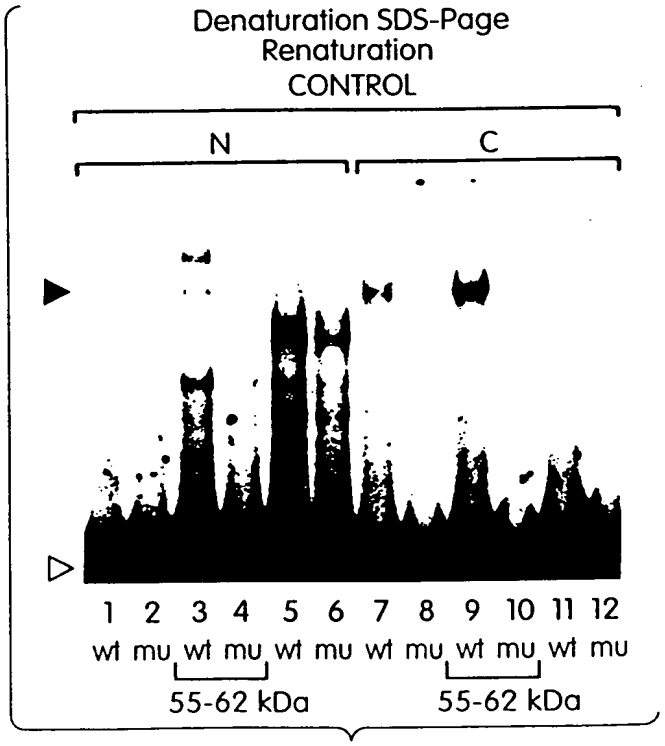


Fig. 27C

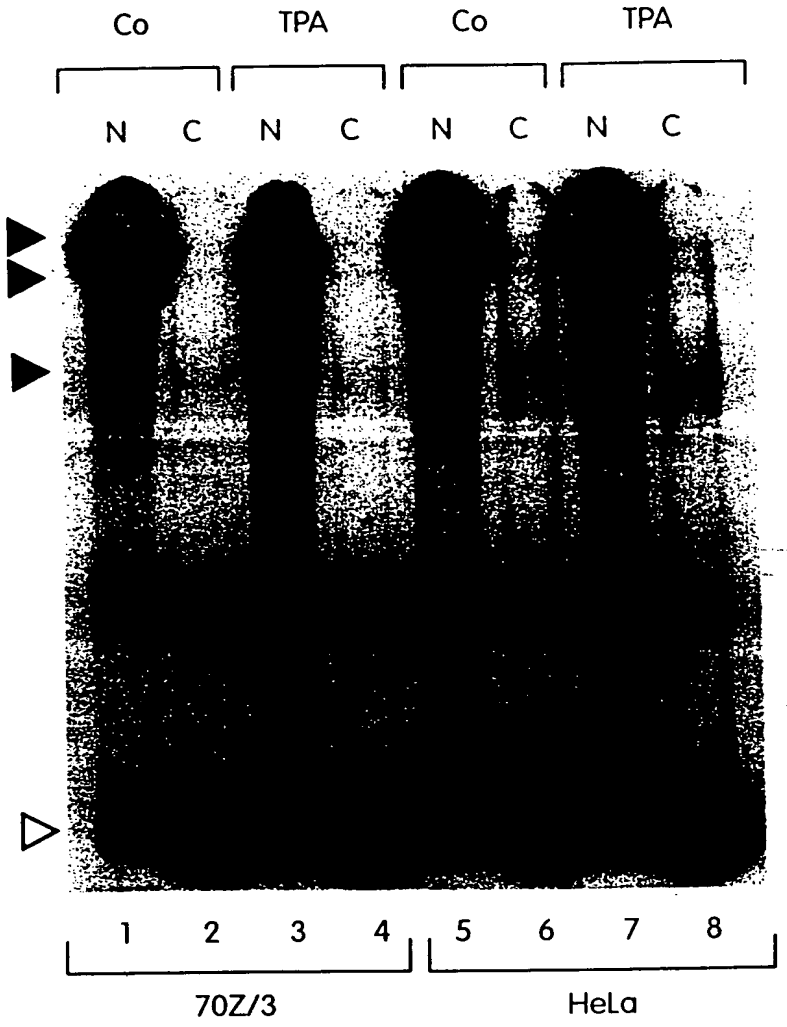


Fig. 28

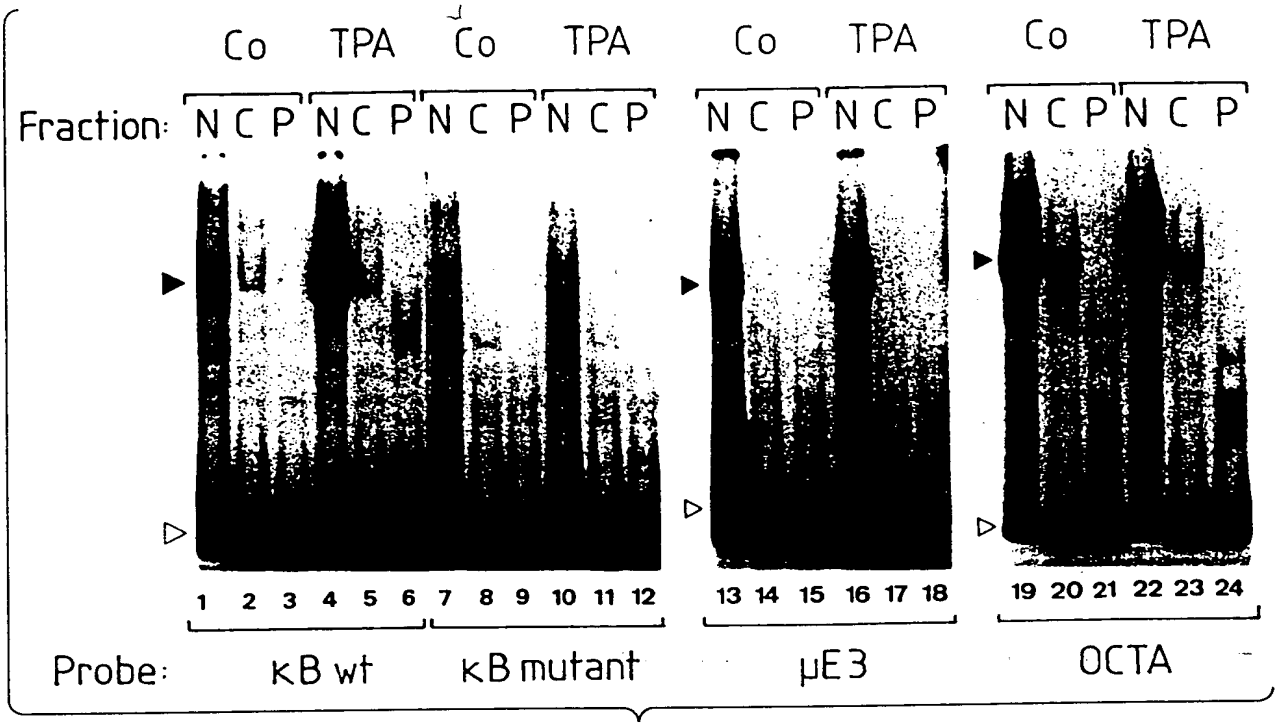

Co
TPA
Co
TPA
Co
TPA
Co
TPA
Fraction: N C P N C P N C P N C P N C P N C P N C P N C P
1 2 3 4 5 6 7 8 9 10 11 12
13 14 15 16 17 18
19 20 21 22 23 24
Probe: κB wt
κB mutant
μE3
OCTA

Fig. 29

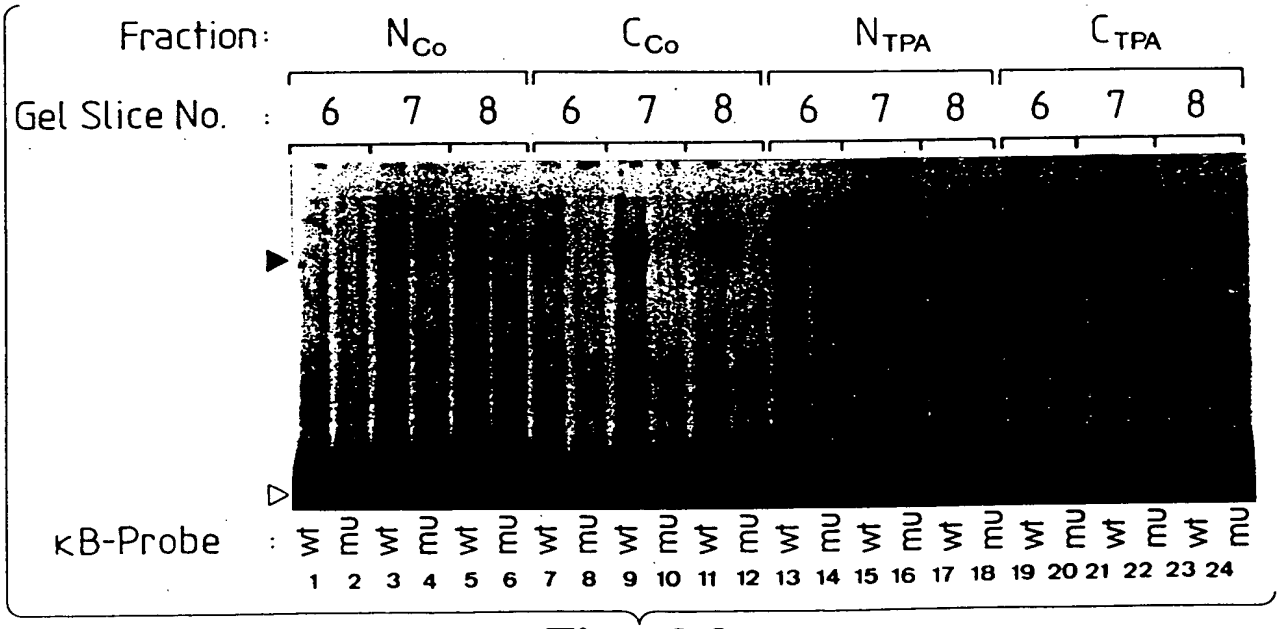

Fraction: N_{Co} C_{Co} N_{TPA} C_{TPA}
Gel Slice No. : 6 7 8 6 7 8 6 7 8 6 7 8
κB-Probe : wt mu wt mu wt mu wt mu wt mu wt mu wt mu wt mu wt mu wt mu wt mu wt mu
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

Fig. 30

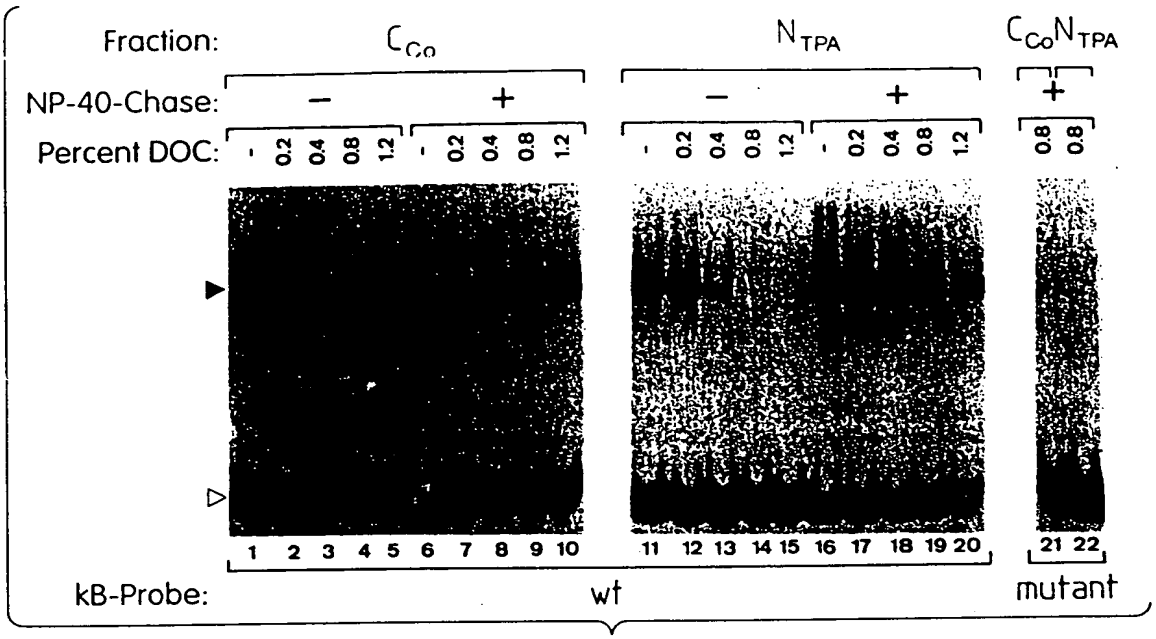


Fig. 31A

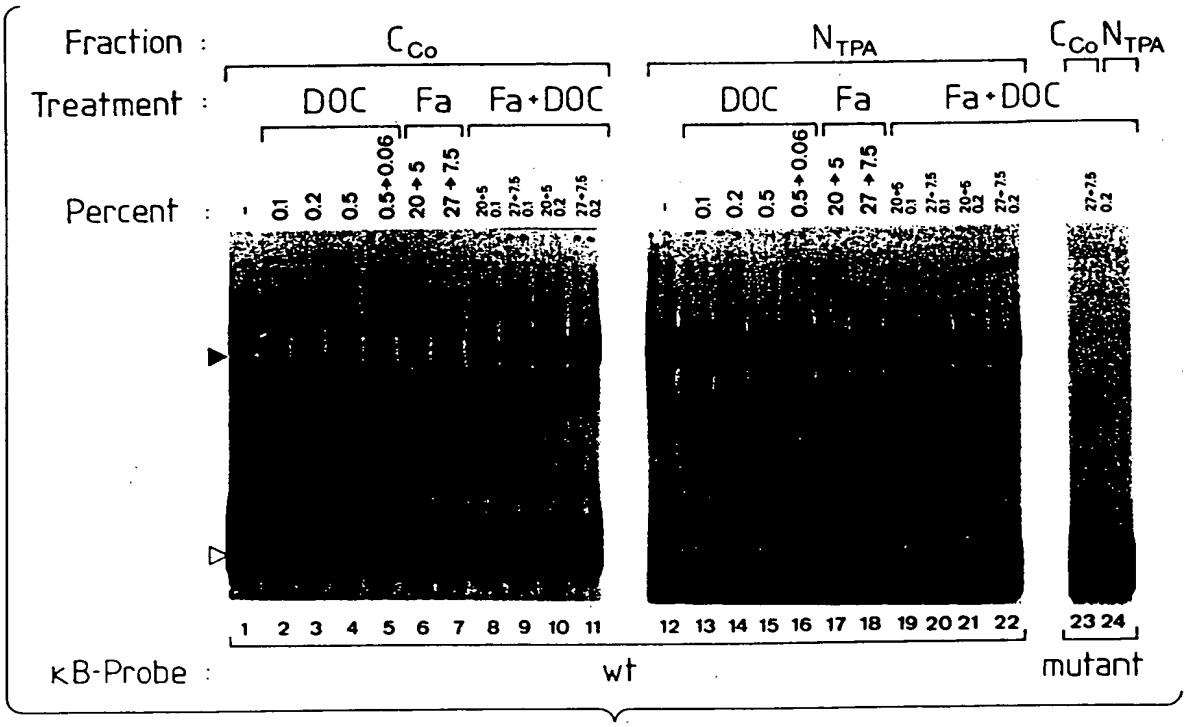


Fig. 31B

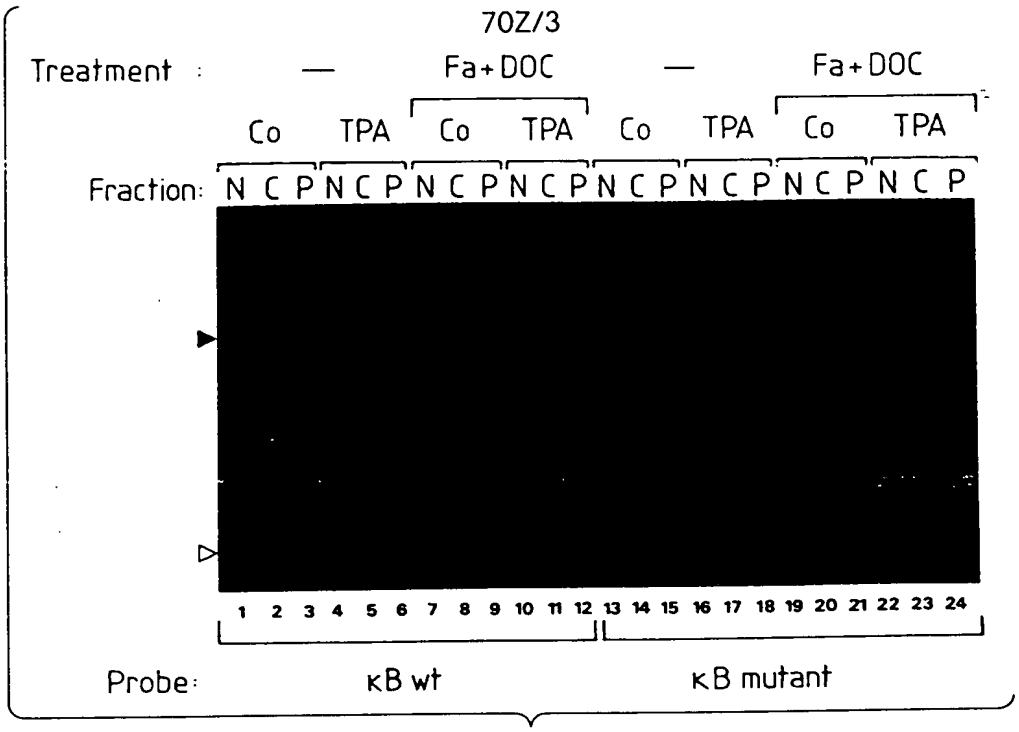

70Z/3
Treatment :
—
Fa+DOC
—
Fa+DOC
Co
TPA
Co
TPA
Co
TPA
Co
TPA
Fraction:
N C P N C P N C P N C P N C P N C P N C P N C P
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
Probe:
κB wt
κB mutant

Fig. 32

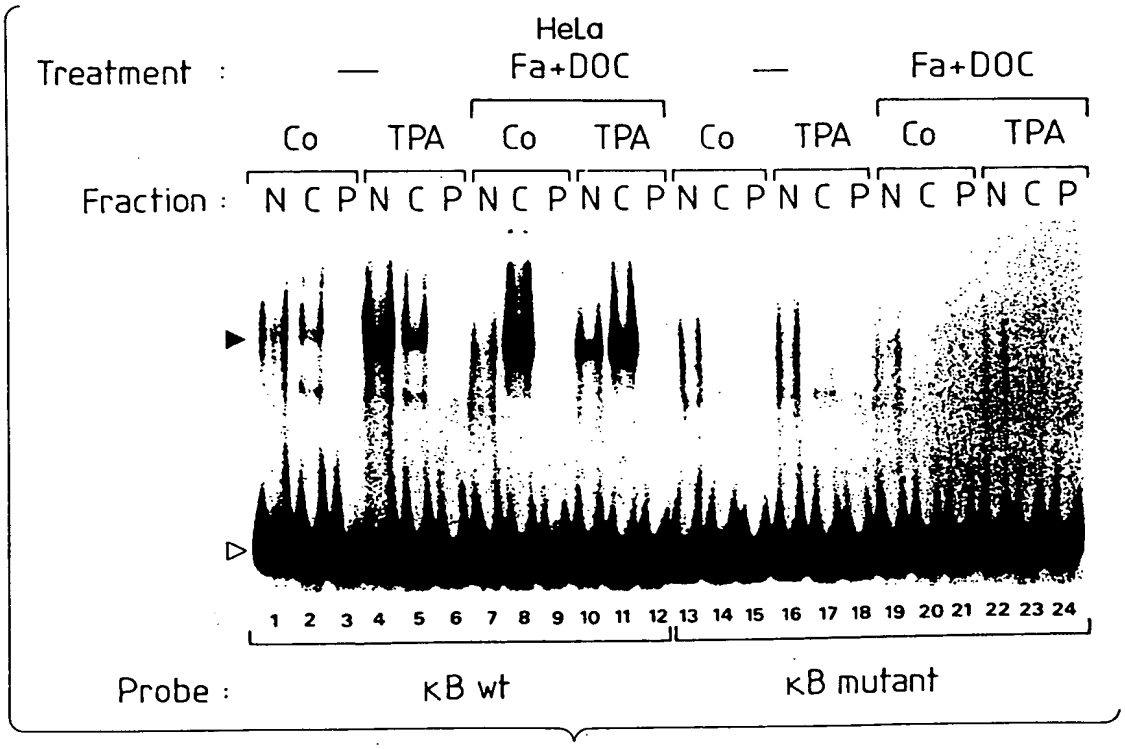

HeLa
Treatment :
—
Fa+DOC
—
Fa+DOC
Co
TPA
Co
TPA
Co
TPA
Co
TPA
Fraction :
N C P N C P N C P N C P N C P N C P N C P N C P
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
Probe :
κB wt
κB mutant

Fig. 33

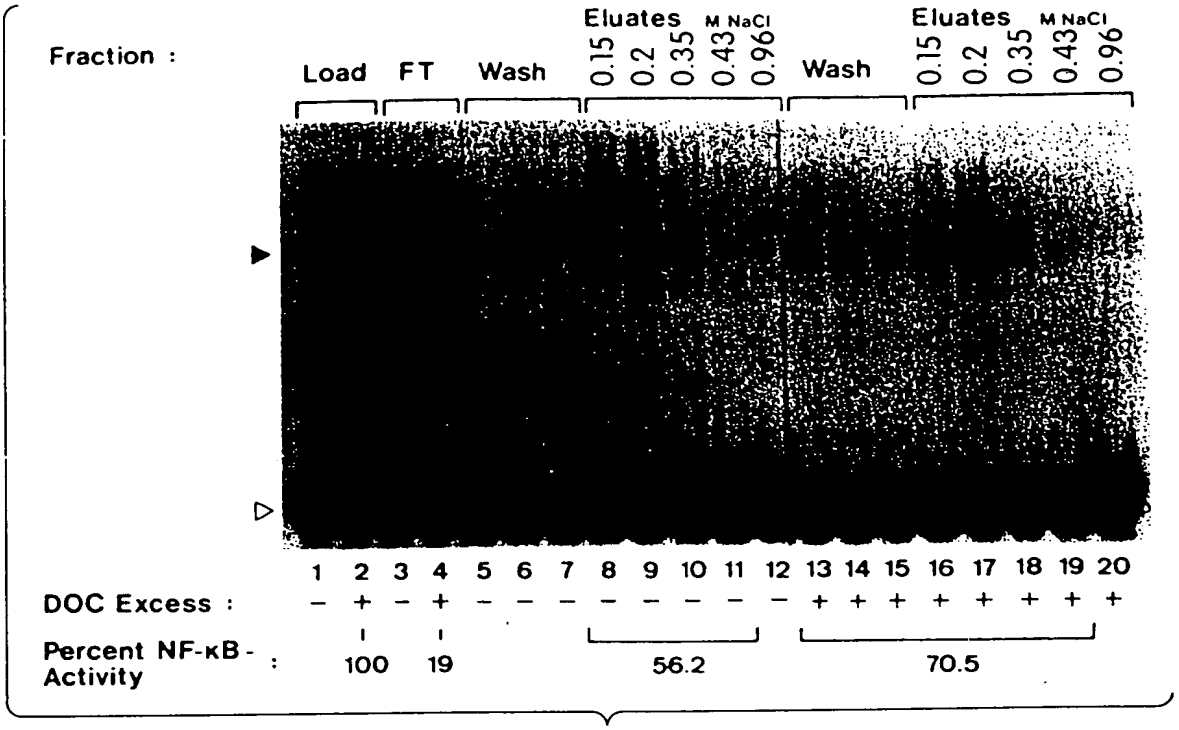


Fig. 34A

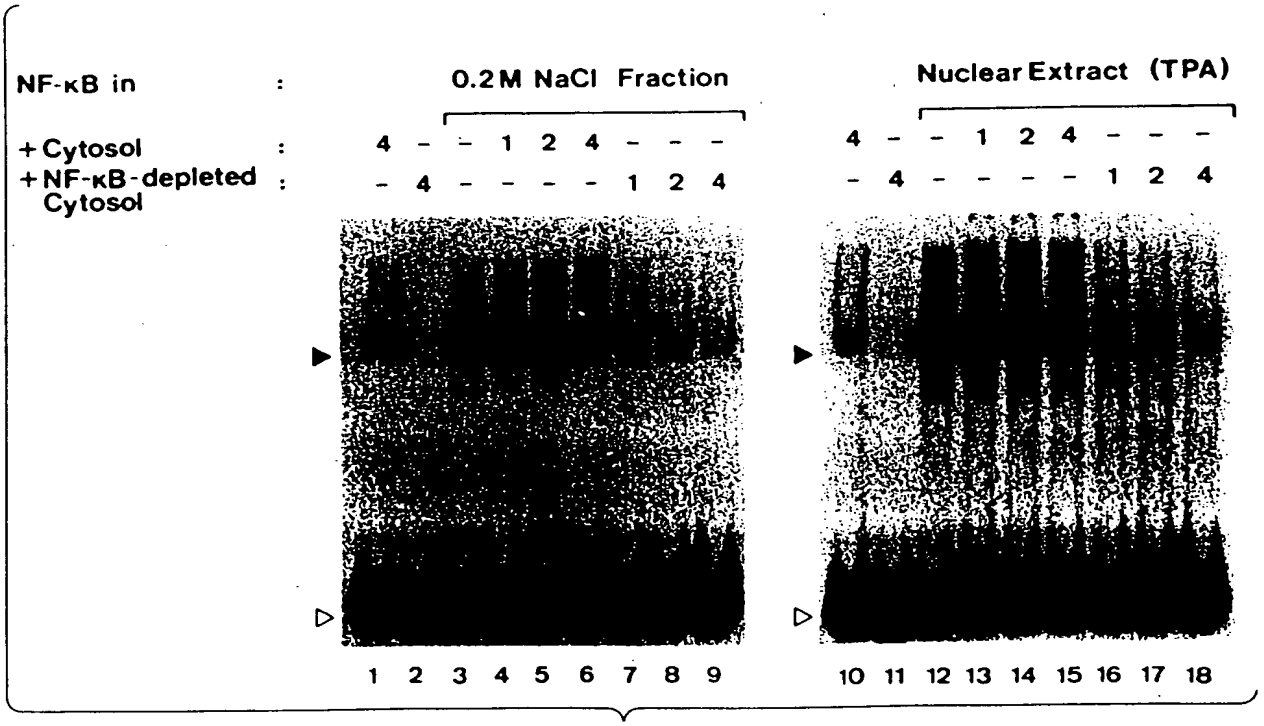


Fig. 34B

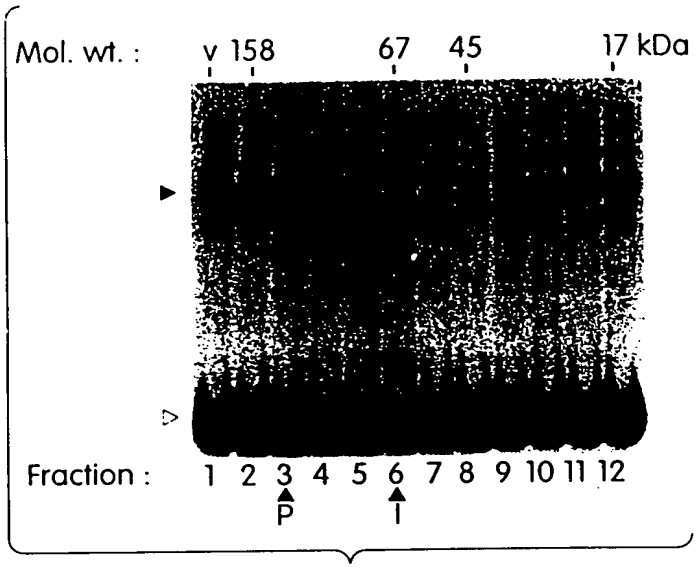


Fig. 35A

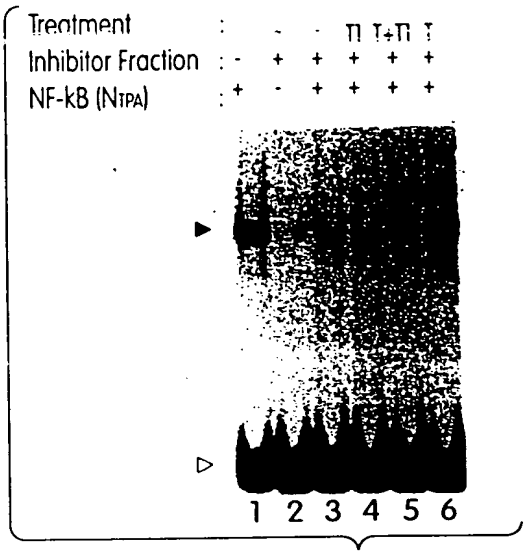


Fig. 35B

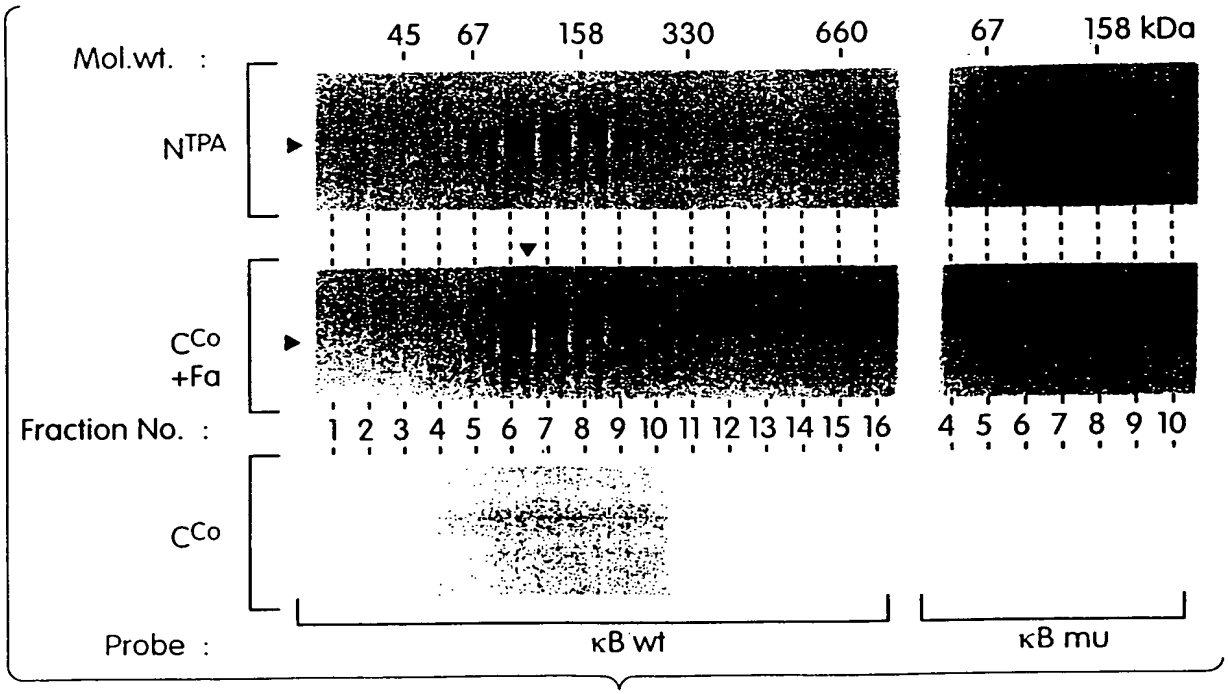


Fig. 35C

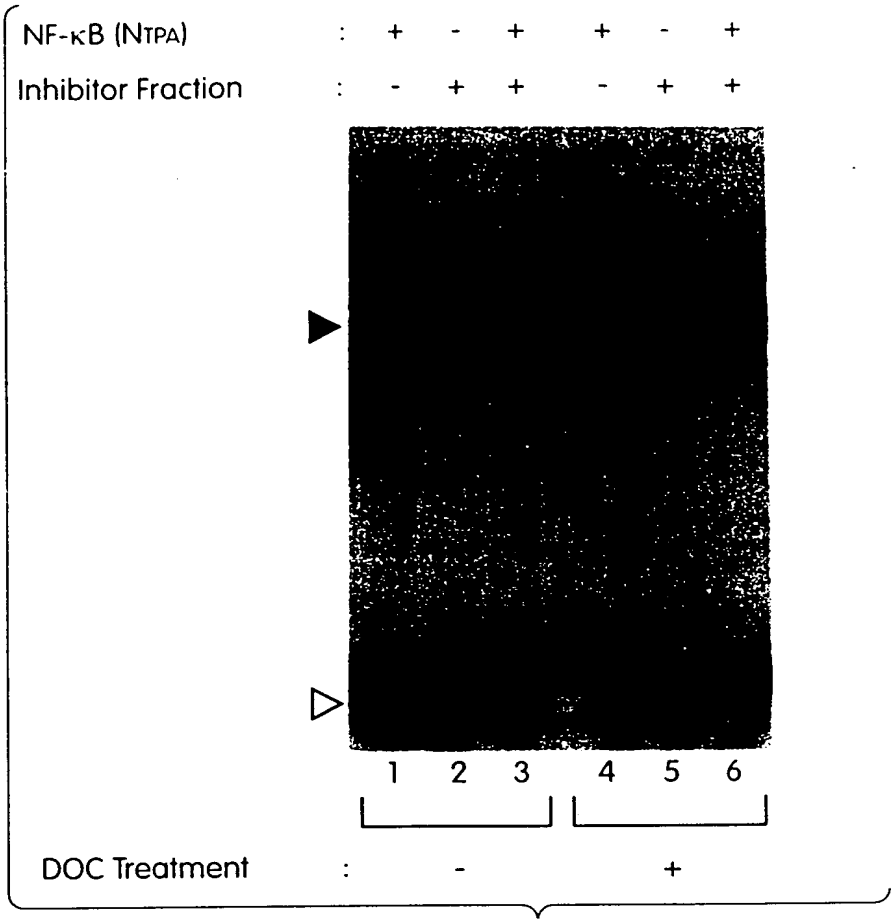


Fig. 36A

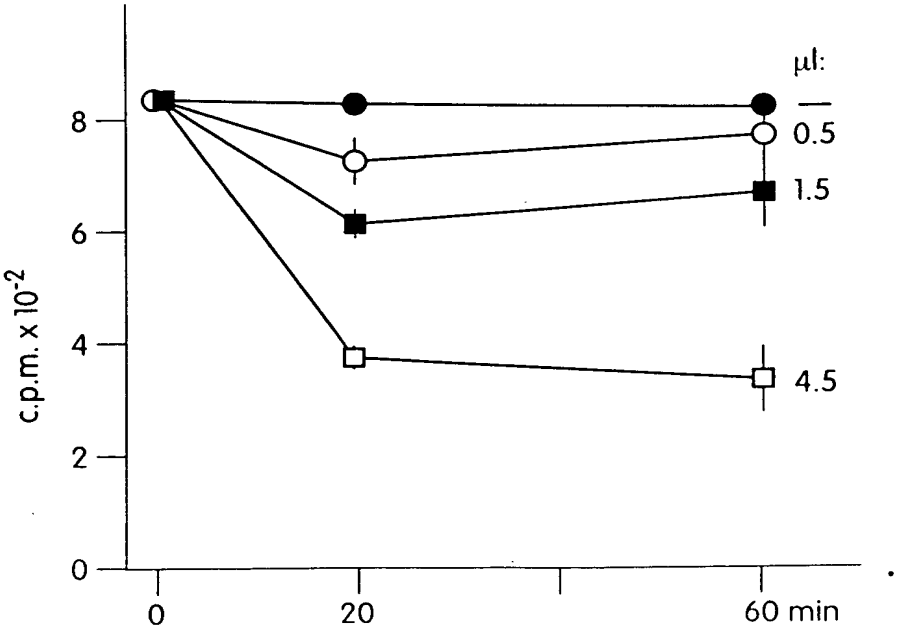


Fig. 36B

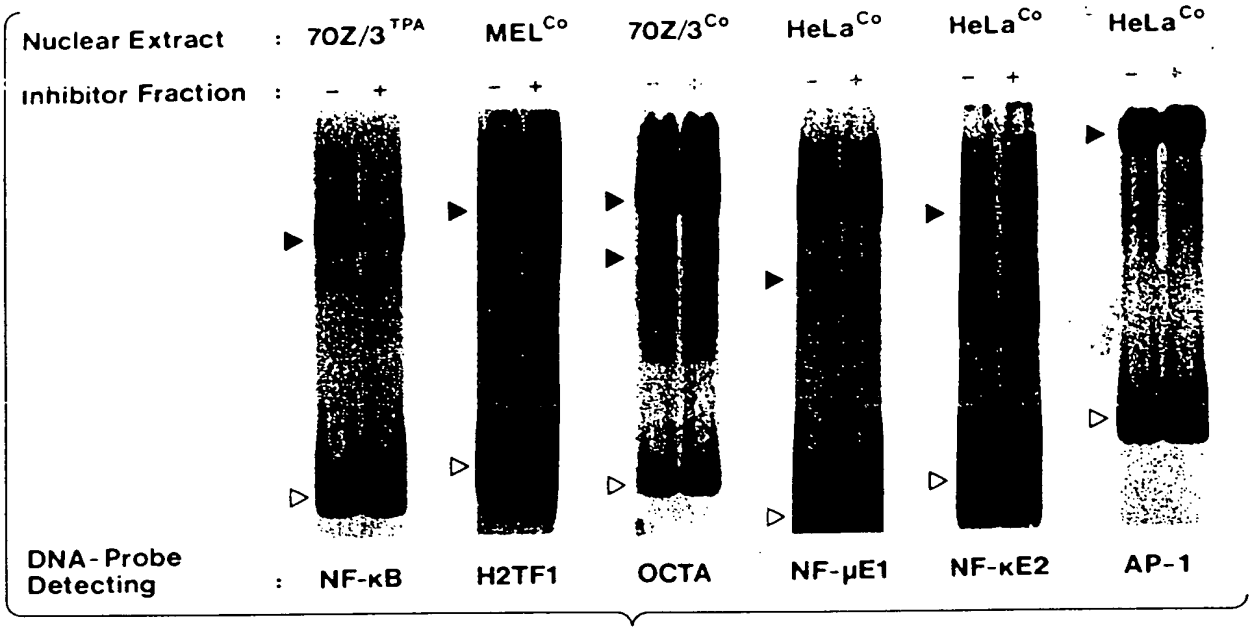


Fig. 37A

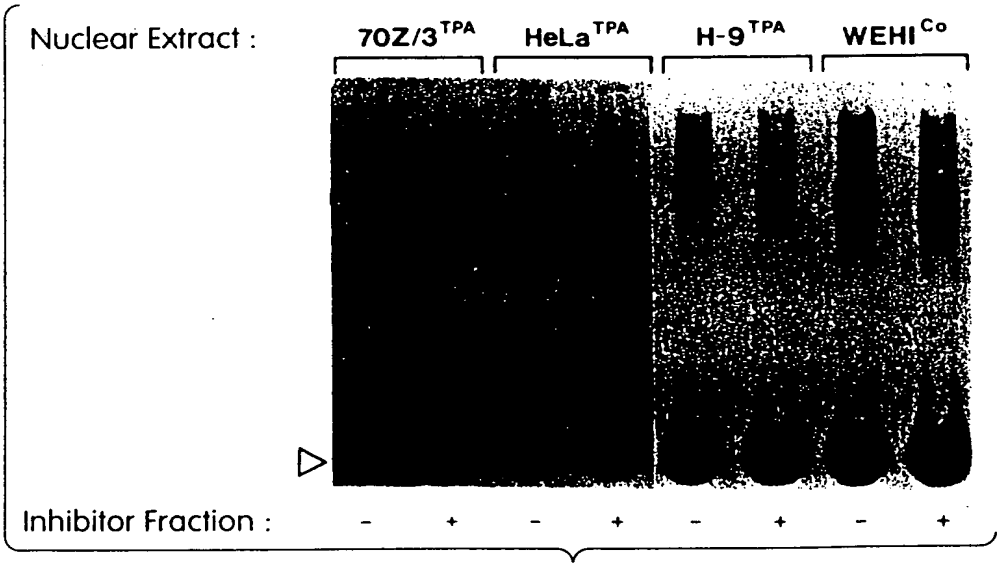


Fig. 37B

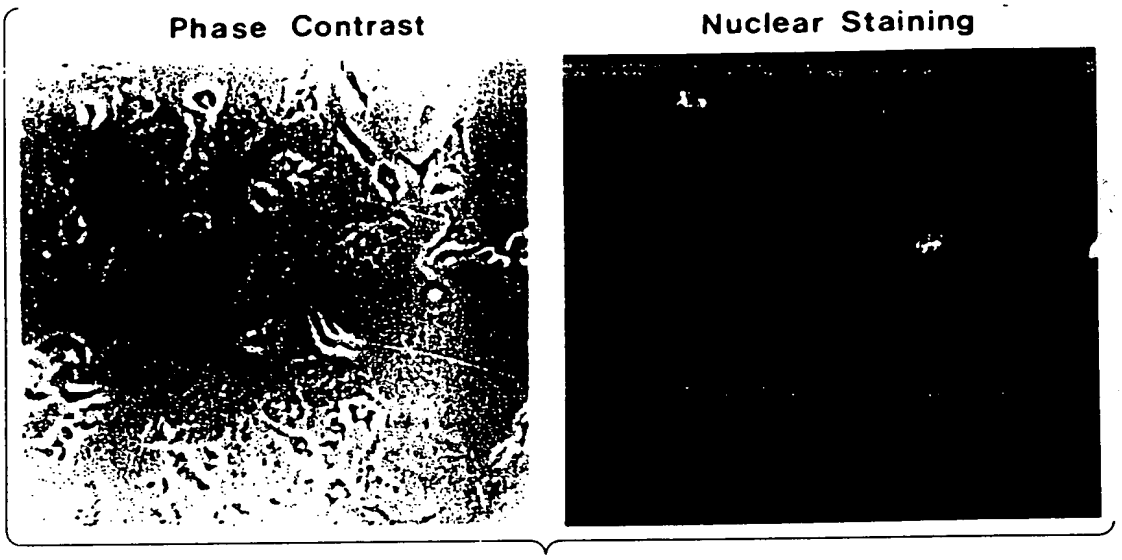


Fig. 38A

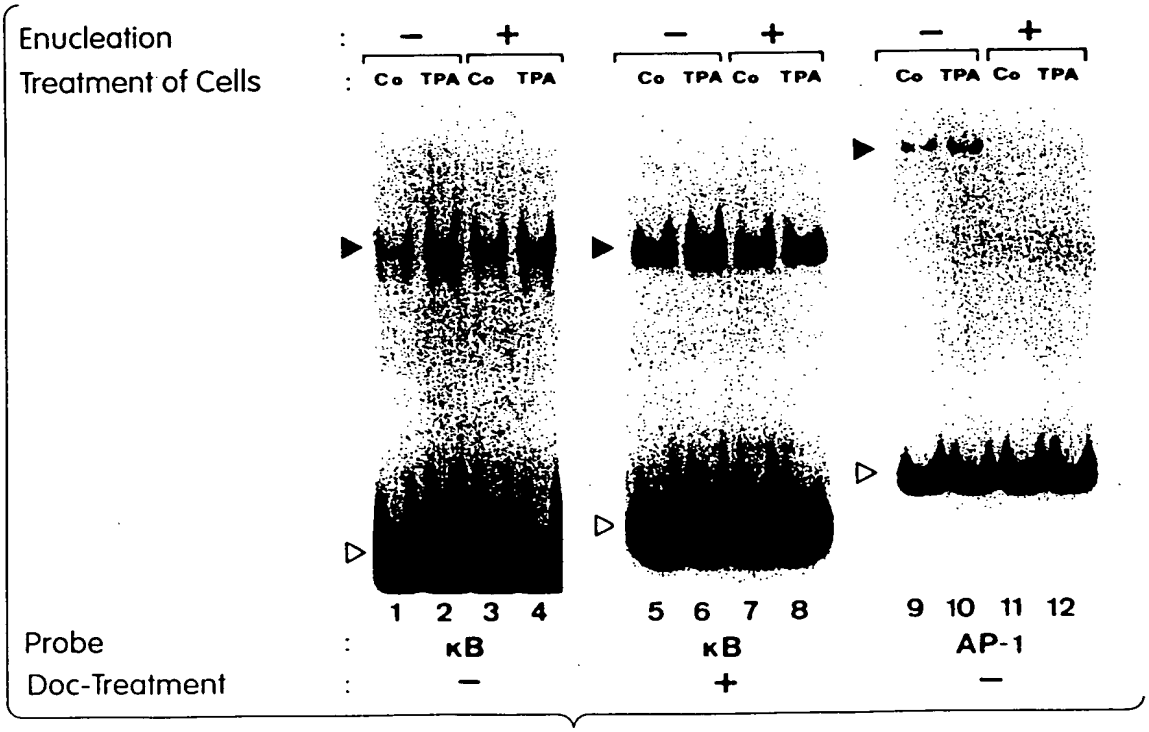


Fig. 38B

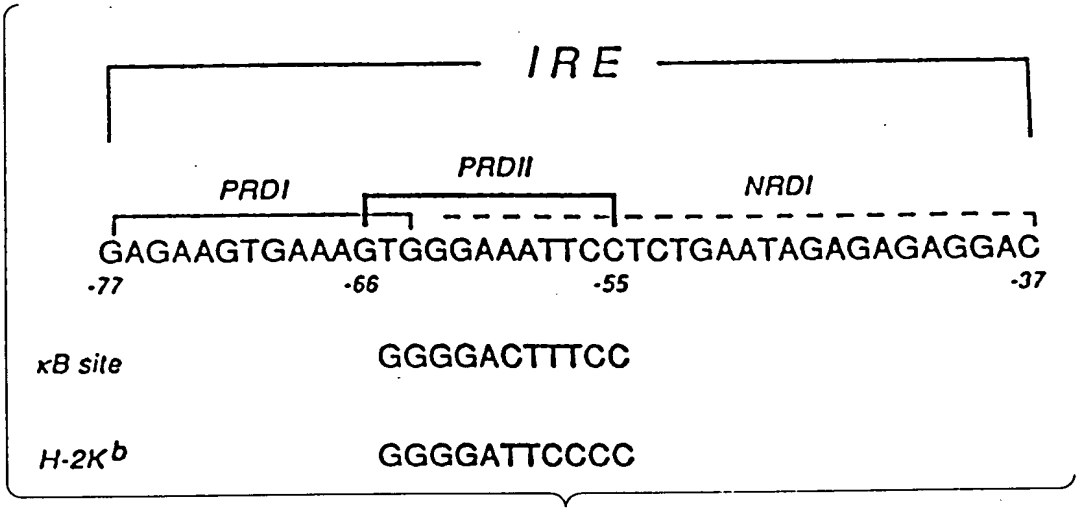

IRE
PRDI
PRDII
NRDI
GAGAAGTGAAAGTGGGAAATTCCTCTGAATAGAGAGAGGAC
-77
-66
-55
-37
κB site
GGGGACTTTCC
H-2K^b
GGGGATTCCCC

Fig. 39

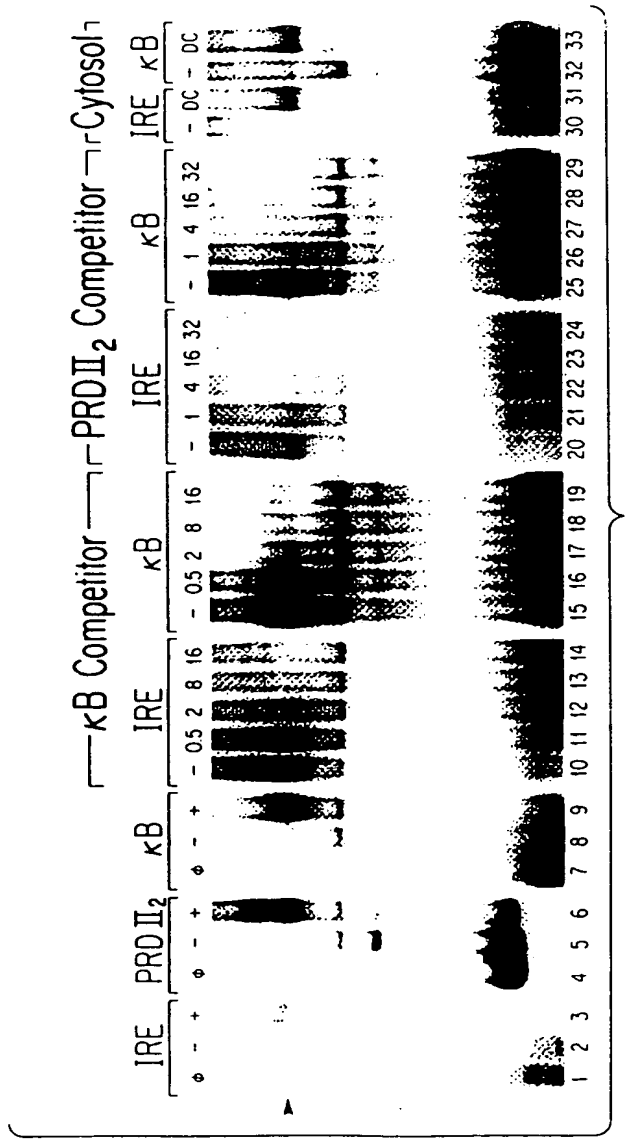


Fig. 40A

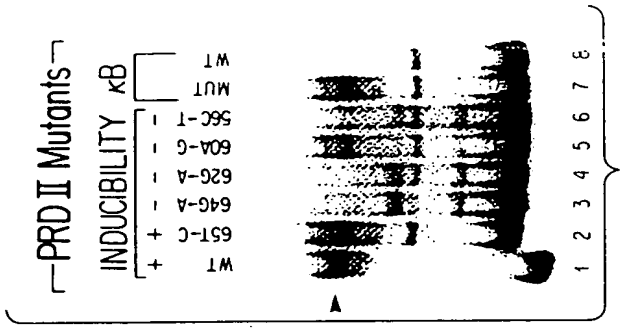


Fig. 40B

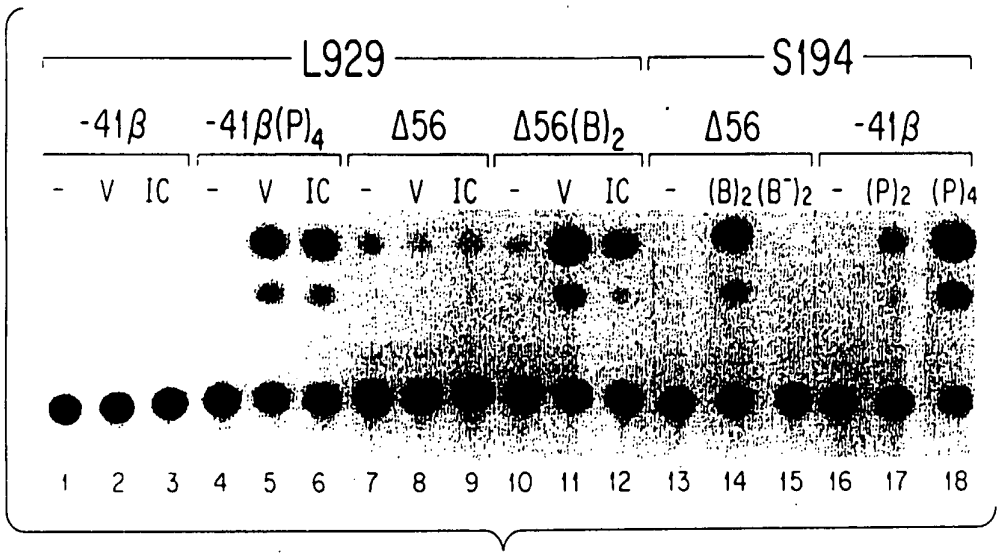


Fig. 41A

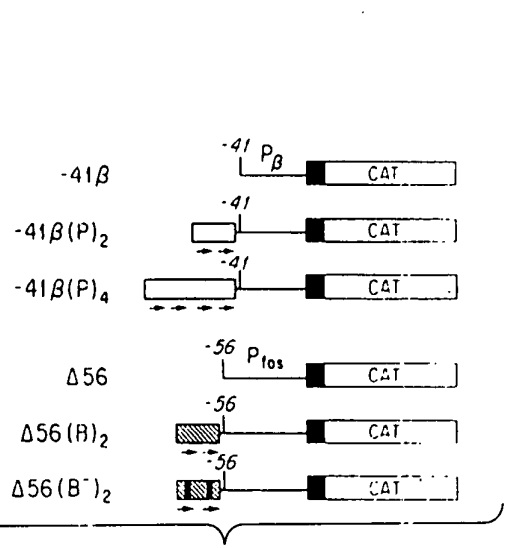


Fig. 41B

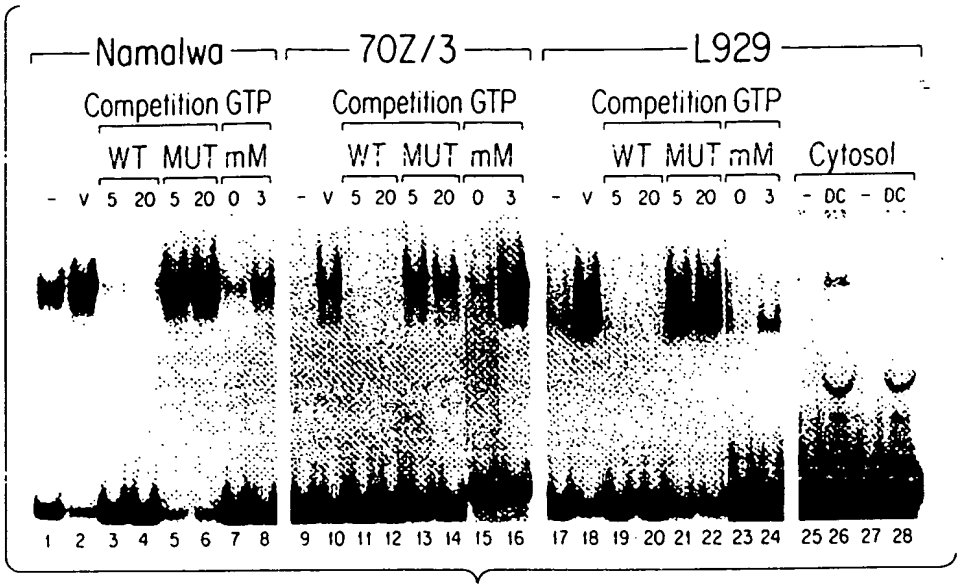


Fig. 42A

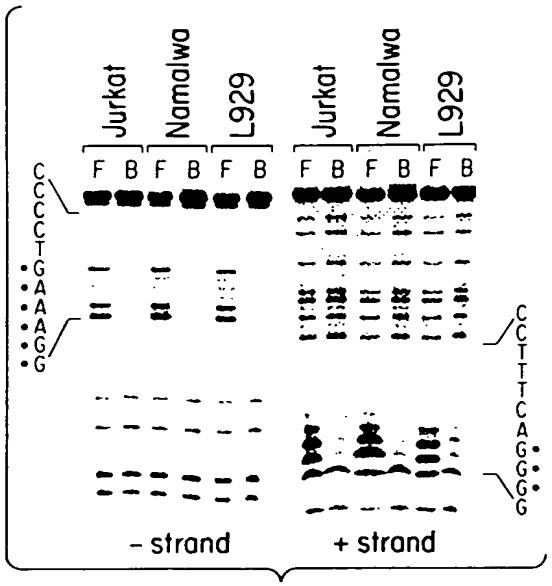


Fig. 42B

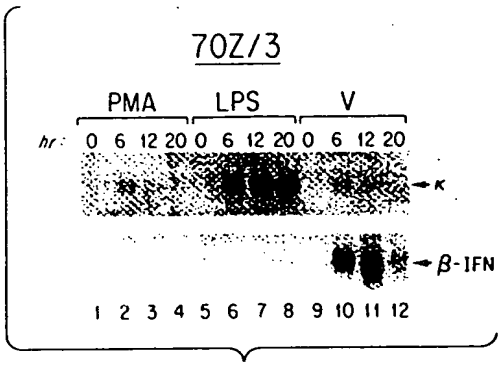


Fig. 42C

Figure 43

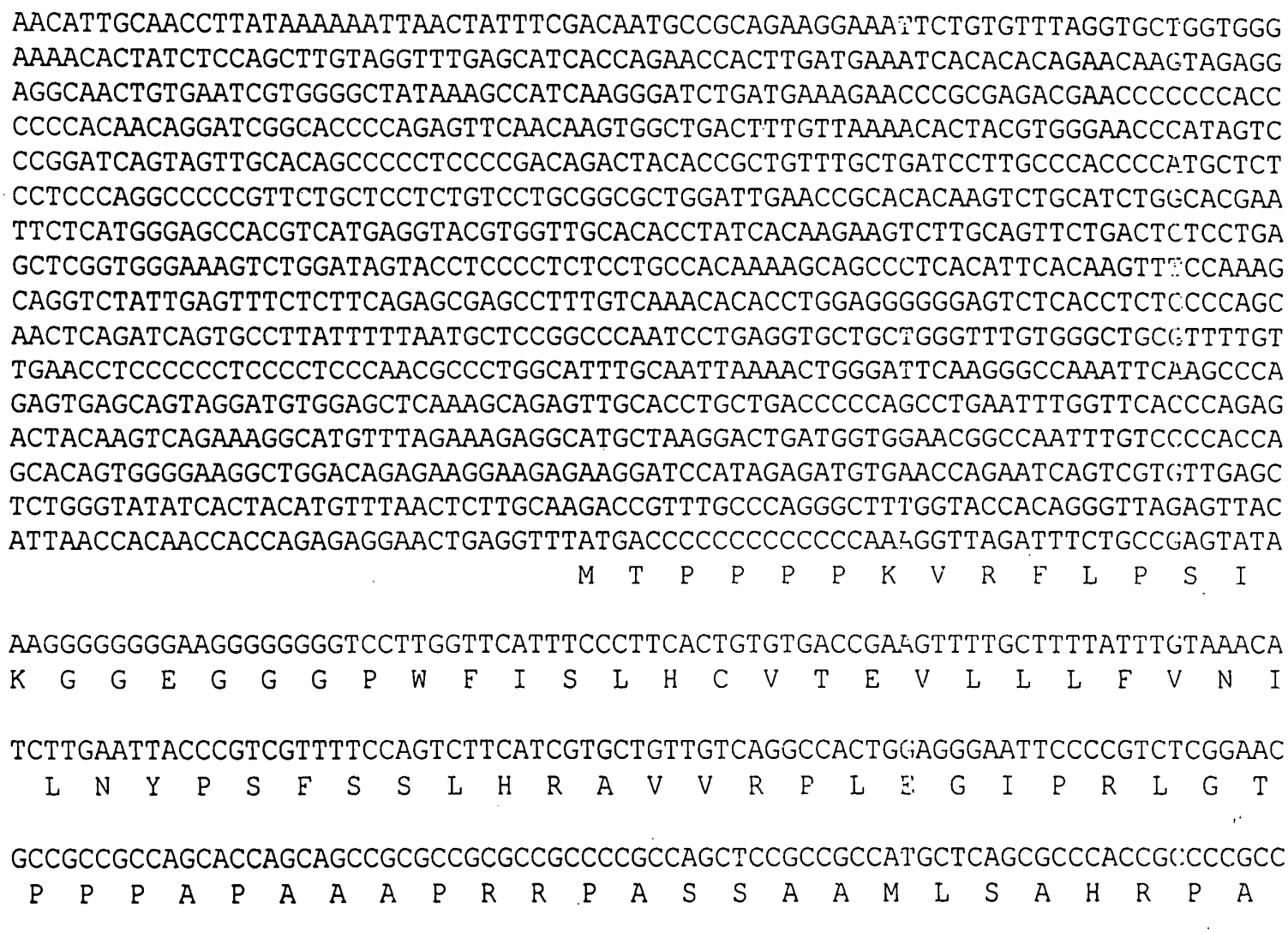

AACATTGCAACCTTATAAAAAATTAACTATTTCGACAATGCCGCAGAAGGAAATTCTGTGTTTAGGTGCTGGTGGG
AAAACACTATCTCCAGCTTGTAGGTTTGAGCATCACCAGAACCACTTGATGAAATCACACACAGAACAAGTAGAGG
AGGCAACTGTGAATCGTGGGGCTATAAAGCCATCAAGGGATCTGATGAAAGAACCCGCGAGACGAACCCCCCCACC
CCCCACAACAGGATCGGCACCCCAGAGTTCAACAAGTGGCTGACTTTGTTAAAACACTACGTGGGAACCCATAGTC
CCGGATCAGTAGTTGCACAGCCCCCTCCCCGACAGACTACACCGCTGTTTGCTGATCCTTGCCCACCCCATGCTCT
CCTCCCAGGCCCCCGTTCTGCTCCTCTGTCCTGCGGCGCTGGATTGAACCGCACACAAGTCTGCATCTGGCACGAA
TTCTCATGGGAGCCACGTCATGAGGTACGTGGTTGCACACCTATCACAAGAAGTCTTGCAGTTCTGACTCTCCTGA
GCTCGGTGGGAAAGTCTGGATAGTACCTCCCCTCTCCTGCCACAAAAGCAGCCCTCACATTCACAAGTTTCCAAAG
CAGGTCTATTGAGTTTCTCTTCAGAGCGAGCCTTTGTCAAACACACCTGGAGGGGGGAGTCTCACCTCTCCCCAGC
AACTCAGATCAGTGCCTTATTTTTAATGCTCCGGCCCAATCCTGAGGTGCTGCTGGGTTTGTGGGCTGCGTTTTGT
TGAACCTCCCCCCTCCCCTCCCAACGCCCTGGCATTTGCAATTAAAACTGGGATTCAAGGGCCAAATTCAAGCCCA
GAGTGAGCAGTAGGATGTGGAGCTCAAAGCAGAGTTGCACCTGCTGACCCCCAGCCTGAATTTGGTTCACCCAGAG
ACTACAAGTCAGAAAGGCATGTTTAGAAAGAGGCATGCTAAGGACTGATGGTGGAACGGCCAATTTGTCCCCACCA
GCACAGTGGGGAAGGCTGGACAGAGAAGGAAGAGAAGGATCCATAGAGATGTGAACCAGAATCAGTCGTGTTGAGC
TCTGGGTATATCACTACATGTTTAACTCTTGCAAGACCGTTTGCCCAGGGCTTTGGTACCACAGGGTTAGAGTTAC
ATTAACCACAACCACCAGAGAGGAACTGAGGTTTATGACCCCCCCCCCCCCAAAGGTTAGATTTCTGCCGAGTATA
M T P P P P K V R F L P S I
AAGGGGGGGGAAGGGGGGGGTCCTTGGTTCATTTCCCTTCACTGTGTGACCGAAGTTTTGCTTTTATTTGTAAACA
K G G E G G G P W F I S L H C V T E V L L L F V N I
TCTTGAATTACCCGTCGTTTTCCAGTCTTCATCGTGCTGTTGTCAGGCCACTGGAGGGAATTCCCCGTCTCGGAAC
L N Y P S F S S L H R A V V R P L E G I P R L G T
GCCGCCGCCAGCACCAGCAGCCGCGCCGCGCCGCCCCGCCAGCTCCGCCGCCATGCTCAGCGCCCACCGCCCCGCC
P P P A P A A A P R R P A S S A A M L S A H R P A

Figure 43 (continued)

GAGCCGCCCGCCGTGGAGGGCTGCGAGCCGCCGCGCAAGGAACGGCAAGGCGGGCTGCTGCCGCCCGACGACCGCC
E P P A V E G C E P P R K E R Q G G L L P P D D R H

ACGACAGCGGGCTGGACTCCATGAAGGAGGAGGAGTACAGGCAGCTGGTGCGGGAGCTGGAGGACATCCGCCTGCA
D S G L D S M K E E E Y R Q L V R E L E D I R L Q

GCCCCGCGAGCCGCCCGCCCGGCCGCACGCCTGGGCCCAGCAGCTCACCGAGGACGGCGACACTTTTCTCCACTTG
P R E P P A R P H A W A Q Q L T E D G D T F L H L

GCGATCATTCACGAGGAAAAGGCCCTGAGCCTGGAGGTGATCCGGCAGGCCGCTGGGGACGCCGCCTTCCTGAACT
A I I H E E K A L S L E V I R Q A A G D A A F L N F

Ank. I

TCCAGAACAACCTCAGCCAGACTCCGCTCCACCTGGCGGTGATCACGGACCAGGCCGAAATCGCCGAGCACCTGCT
Q N N L S Q T P L H L A V I T D Q A E I A E H L L

Ank. II

GAAGGCTGGCTGCGACCTGGATGTCAGGGACTTCCGTGGGAACACCCCGCTCCACATCGCCTGCCAGCAGGGCTCG
K A G C D L D V R D F R G N T P L H I A C Q Q G S

Ank. III

CTCCGCAGCGTCAGTGTCCTCACGCAGCACTGCCAGCCCCACCACCTCCTCGCCGTCCTGCAGGCCACCAACTACA
L R S V S V L T Q H C Q P H H L L A V L Q A T N Y N

ACGGCCATACATGTCTCCATTTGGCATCTATTCAAGGATACCTGGCTGTTGTCGAATACCTGCTGTCCTTAGGAGC
G H T C L H L A S I Q G Y L A V V E Y L L S L G A

Ank. IV

AGATGTAAATGCTCAGGAGCCATGCAATGGGAGAACAGCACTACACTTGGCCGTAGACCTTCAGAACTCAGACCTG
D V N A Q E P C N G R T A L H L A V D L Q N S D L

Ank. V

Figure 43 (continued)

GTGTCACTTCTGGTGAAACACGGGCCAGATGTGAACAAAGTGACCTACCAGGGCTACTCCCCATACCAGCTTACAT
V S L L V K H G P D V N K V T Y Q G Y S P Y Q L T W

GGGCAGAGACAACGCCAGCATACAGGAGCAGCTGAAGCTGCTGACCACAGCTGACCTGCAGATACTGCCCGAAAGT
A E T T P A Y R S S 354

GAGGATGAGGAGAGCAGTGAATCAGAGCCAGAGTTCACAGAGGATGAACTTATGTATGATGACTGCTGTATTGGAG
GAAGACAGCTGACATTTTAAAGCAGAGGTTTCTGTGAGAAGTGACTGTGTACATATGTATAGGAAAAAAAGCCTGA
CTTTCTTCATTTAAAAAGAAAGTCTATACTCGAAGGAGAAAAAAGTACTGAGATACTACACTGCCCAGCCAGGAGC
ACATCATGCTAACAGGTTCCATGCTCTGACCTGTACTTAAGTAACGGGATGGGATGTGTAACATCGTTAAGAGATC
AGTGAACATGCACACCATCTGATAAAGAGCCACGTTATCTAATTTCTCTGCCACATGAGGATAACGGACTGCACGT
CCAATGTGCTGTTGTCAGAAATGCGTTTGAGAGCTGCCTTGTGACACTAAGTGCTGTGAGGAGTGCTCATCCCCCT
CGGTGGCAAGACAGGCTTGCACAAACGTCCCATCTGCTTGAAGACTGTGAGGTTGGCATTAGGTTGAGGCACTGCT
GTGCCCTGCTCCCTGACCCTGGCTGCTCAGGGTTGAGGAGTCCGACCATGGGAGAGGTGACCTGGCTGCTGGGAGG
AAGGTAGCAATGATGTTAACTGTGGGCATTTGGAAACTGTGTGTTTCACACCATGTGTGTCATAATTGCTACACTT
TTTAGCAACTGTATAGAATGTAAATACTGTACATCTTTGTTTATAATTATTTTGGTACCTGTGAGATATGTATTTA
TTAAAAAAGGCAGATTTCTGTAAAAAA